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(54) Title: CODON-OPTIMIZED POLYNUCLEOTIDE-BASED VACCINES AGAINST BACILLUS ANTHRACIS INFECTION

(57) Abstract: The invention is related to polynucleotide-based anthrax vaccines. In particular, the invention is plasmids operably encoding Bacillus anthracis antigens, in which the naturally-occurring coding regions for the B. anthracis antigens have been modified for improved translation in human or other mammalian cells through codon optimization. In certain embodiments, the coding regions are also modified so as to remove potential N-linked glycosylation sites. B. anthracis antigens which are useful in the invention include, but are not limited to protective antigen (PA), lethal factor (LF), and fragments, variants or derivatives of either of these antigens. The invention is further directed to methods to induce an immune response to B. anthracis in a mammal, for example, a human, comprising delivering a plasmid encoding a codon-optimized B. anthracis antigen as described above. The invention is also directed to pharmaceutical compositions comprising plasmids encoding a codon-optimized B. anthracis antigen as described above, and further comprising adjuvants, excipients, or immune modulators.

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CODON-OPTIMIZED POLYNUCLEOTIDE-BASED VACCINES
AGAINST *BACILLUS ANTHRACIS* INFECTION

BACKGROUND OF THE INVENTION

5 Field of the Invention

Historically, anthrax infection is associated with herd animals and was not commonly seen as a human pathogen (Mock, M. and Fouet, A. *Annual Review of Microbiology* 55:647-671(2001)). Therefore, it is not surprising that zoonotic *Bacillus anthracis* infection and pathogenesis in humans is not well characterized. However, anthrax has become a greater human disease problem with the realization that anthrax spores could be weaponized. It is now widely accepted that *B. anthracis* spores can be inexpensively produced, are extremely stable when properly stored, and could be effectively distributed in populated areas. Consequently, *B. anthracis* becomes an ideal organism for use as a biological weapon and opens up the possibility of an intentional and major outbreak of infection in humans. Research during the past 10-15 years has provided an increasing amount of information about the molecular basis of disease in humans, providing the scientific basis for developing specific diagnostics and defined subunit vaccines.

20 Related Art

In addition to developing more rapid and sensitive diagnostics, molecular biological methods enable the development of defined subunit vaccines to counter bioterrorism. Indeed, safe, effective recombinant subunit vaccines would significantly reduce, and perhaps eliminate, the need for therapeutic treatments. In the case of *B. anthracis*, virulence is the results of a multi-component toxin secreted by the organism. The toxin consists of three separate gene products designated protective antigen (PA), lethal factor (LF) and edema factor (EF). The genes encoding these toxin components (pag, lef, and cya, respectively) are located on a 184-kb plasmid designated pXO1.

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pXO1, along with a second plasmid, pXO2 carrying capsule genes thought to protect bacilli from host cell phagocytosis, are required for full anthrax virulence and are carried by all virulent strains of *B. anthracis* (Mikesell, P., *et al. Infect. Immun.* 39: 371-376 (1983)). PA (735 aa, MW 82,684) is a single chain protein which binds to a mammalian cell surface receptor. Upon cleavage by furin (or a furin-like enzyme activity), it is cleaved into a 63-kDa receptor-bound product (Leppla, S.H., "Production and purification of anthrax toxin," in *Methods in Enzymology*. S. Harshman, ed., Academic Press, Inc., Orlando, FL (1988), pp. 103-116; Klimpel, K.R., *et al., Proc. Natl. Acad. Sci. (USA)* 89:10277-10281 (1992); Gordon, V.M., *et al., Infect. Immun.* 63:82-87 (1995); Petosa, C., *et al., Nature* 385:8833-8838 (1997)). The 63-kDa PA fragment forms a heptameric complex on the mammalian cell surface which is capable of interacting with the 90-kDa LF protein and the 89-kDa EF protein, which are subsequently internalized (Milne, J.C., *et al., J. Biol. Chem.* 269:20607-20612 (1994); Petosa, C., *et al., Nature* 385:8833-8838 (1997)). LF (776 aa, MW 90,237) is a zinc metalloprotease that cleaves several isoforms of MAP kinase kinase (Mek1, Mek2, MKK3), thereby disrupting signal transduction events within the cell and eventually leading to cell death (Duesbery, N.S., *et al., Science* 280:734-737 (1998); Pellizari, R., *et al., FEBS Ltrs* 462:199-204. (1999)). The EF protein (767 aa, MW 88,808) is a calmodulin-dependent adenylate cyclase that causes deregulation of cellular physiology, leading to clinical manifestations that include edema (Leppla, S.H., *Proc. Natl. Acad. Sci. (USA)* 79:3162-3166 (1982)). The LF protein, which together with PA is referred to as lethal toxin (Letx), is considered responsible for the rapid lethality of anthrax infection (Pannifer, A., *et al., Nature* 414:229-232. (2001)).

Protection against anthrax infection is associated with a humoral immune response directed against PA (Ivins, B.E. and Welkos, S.L., *Eur. J. Epidemiol.* 4(1):12-19 (1988); Ivins, B., *et al., Vaccine* 13:1779-1784 (1995)). Some evidence suggests that EF and LF may also contribute to specific immunity (Little, S.F. and Knudson, G.B., *Infect. Immun.* 52:509-512. (1986);

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Ivins, B.E. and Welkos, S.L., *Eur. J. Epidemiol.* 4(1):12-19 (1988); Pezard, C., *et al., Infect. Immun.* 63:1369-1372 (1995)), although these components have not been formulated into a subunit vaccine.

5 The current FDA-approved anthrax vaccine, Anthrax Vaccine Adsorbed (AVA), is produced from the culture supernatant fraction of the V770-NP1-R strain of *B. anthracis*. Its principal component is the PA antigen adsorbed onto aluminum hydroxide. The production process is complex and the precise composition of the bacterial cell supernatant is not well characterized. Consequently, there is a significant lot-to-lot variation. In addition, the approved vaccination regimen is less than optimal for compliance and convenience: AVA is administered subcutaneously in a 0.5 ml volume, at 10 0, 2, and 4 weeks and then again at 6, 12, and 18 months. Annual boosts are also required.

15 Recently there has been a report of potential safety concerns in pregnant women, although the causal relationship has not been well established. As a result of these and other lay press reports, there is a negative public perception about the reliability and quality of the AVA vaccine even though the actual safety of the vaccine has never been seriously questioned in the scientific literature. A major concern with the current AVA anthrax vaccine is the paucity of analytical characterization of the actual composition 20 of the vaccine preparation. It has been suggested that the presence of minute amounts of unspecified components may contribute to the adverse events that have been associated with administration of the AVA vaccine. In contrast, DNA vaccines are designed to elicit immunity against discrete, well-defined target antigens and are unlikely to be the subject of the same criticism. In 25 short, DNA vaccines can be multivalent and yet highly defined.

During the past few years there has been substantial interest in testing DNA-based vaccines for a number of infectious diseases where the need for a vaccine, or an improved vaccine, exists. Several well-recognized advantages 30 of DNA-based vaccines include the speed, ease and cost of manufacture, the versatility of developing and testing multivalent vaccines, the finding that

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DNA vaccines can produce a robust cellular response in a wide variety of animal models as well as in man, and the proven safety of using plasmid DNA as a delivery vector (Donnelly, J.J., *et al.*, *Annu. Rev. Immunol.* 15:617-648 (1997); Manickan, E., *et al.*, *Crit. Rev. Immunol.* 17(2):139-154 (1997)).

5 DNA vaccines represent the next generation in the development of vaccines (Nossal, G., *Nat. Med.* 4(5 Suppl):475-476 (1998)) and numerous DNA vaccines are in clinical trials.

DNA-based immunization have already been shown, in animal models, to protect against a lethal challenge of anthrax toxin. The initial published
10 work indicated that a plasmid encoding the protease-cleaved fragment (PA₆₃) of PA (Gu, *et al.*, *Vaccine* 17:340-344 (1999)) elicited protective immunity against a lethal toxin challenge. Price, *et al.*, *Infection and Immunity* 69:4509-4515 (2001) extended these observations and demonstrated that DNA-based immunization with a fragment of the LF gene product would also contribute to
15 or provide protection against a lethal toxin challenge. Having established proof of principle in pre-clinical studies, we now propose to develop an aggressive product development plan that will lead to an efficacious human vaccine against *B. anthracis* using a DNA-based immunization strategy.

Retooling coding regions encoding polypeptides from pathogens using
20 codon frequencies preferred in a given mammalian species often results in a significant increase in expression in the cells of that mammalian species, and concomitant increase in immunogenicity. See, *e.g.*, Deml, L., *et al.*, *J. Virol.* 75:10991-11001 (2001), and Narum, DL, *et al.*, *Infect. Immun.* 69:7250-7253 (2001).

25 There remains a need in the art for convenient, safe, and efficacious immunogenic compounds to protect vertebrates against *Bacillus anthracis* infection. The present invention provides safe yet effective immunogenic compounds and methods to protect vertebrates against *Bacillus anthracis* infection using such immunogenic compounds.

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SUMMARY OF THE INVENTION

The present invention is directed to enhancing immune response of a vertebrate in need of protection against anthrax infection by administering *in vivo*, into a tissue of a vertebrate, a polynucleotide comprising a codon-optimized coding region encoding a component of *Bacillus anthracis* lethal toxin or nucleic acid fragments of such coding regions encoding fragments, variants, or derivatives thereof. Nucleic acid fragments of the present invention are altered from their native state in one or more of the following ways. First, a nucleic acid fragment which encodes a component of the *B. anthracis* lethal toxin may be part or all of a codon-optimized coding region, optimized according to codon usage in a given species, *e.g.*, a vertebrate species, *e.g.*, a mammalian species, *e.g.*, humans. In addition, a nucleic acid fragment which encodes a component of the *B. anthracis* lethal toxin may be a fragment which encodes only a portion of a full-length polypeptide, and/or may be mutated so as to, for example, remove from the encoded polypeptide adventitious protein motifs present in the encoded polypeptide or virulence factors associated with the encoded polypeptide. For example, the nucleic acid sequence could be mutated so as not to encode adventitious N-linked glycosylation motifs (N-X-(S or T), where X is any amino acid). The polynucleotides are incorporated into the cells of the vertebrate *in vivo*, and a prophylactically or therapeutically effective amount of a *Bacillus anthracis* lethal toxin component is produced *in vivo*.

The invention further provides immunogenic compositions comprising a polynucleotide which comprises one or more codon-optimized coding regions encoding components of *Bacillus anthracis* lethal toxin or nucleic acid fragments of such coding regions encoding fragments, variants, or derivatives thereof, and methods for enhancing the immune response of a vertebrate to *Bacillus anthracis* infection by administering to the tissues of a vertebrate one or more polynucleotides comprising one or more codon-optimized coding regions encoding components of *Bacillus anthracis* lethal toxin or nucleic acid

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fragments of such coding regions encoding fragments, variants, or derivatives thereof. The present invention further provides plasmids and other polynucleotide constructs for delivery of nucleic acid coding sequences to a vertebrate which provide expression of *Bacillus anthracis* toxin components, or fragments, variants, or derivatives thereof.

In certain embodiments, the invention further provides methods for enhancing the immune response of a vertebrate to *Bacillus anthracis* infection by sequentially administering two or more different immunogenic compositions to the tissues of the vertebrate. Such methods comprise initially administering one or more polynucleotides comprising one or more codon-optimized coding regions encoding components of *Bacillus anthracis* lethal toxin or nucleic acid fragments of such coding regions encoding fragments, variants, or derivatives thereof, to prime immunity, and then administering subsequently a different vaccine composition, for example a recombinant viral vaccine, a protein subunit vaccine, or a recombinant or killed bacterial vaccine or vaccines to boost the anti-*Bacillus anthracis* toxin immune response in the vertebrate.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the nucleotide sequence (SEQ ID NO:1) and amino acid translation (SEQ ID NO:2) of TPA-PA63. SEQ ID NO:1 contains a nucleic acid fragment of a human codon-optimized PA coding region, encoding the 63kD furin cleavage product of the *Bacillus anthracis* protective antigen (PA), fused to a nucleic acid encoding the human tissue plasminogen activator (TPA) signal peptide sequence. Nucleotides 1-12 of SEQ ID NO:1 is a Kozak translation initiation element and nucleotides 13-81 of SEQ ID NO:1 encode the TPA signal peptide. Nucleotides 82-1782 of SEQ ID NO:1 encode the 63kD furin processed fragment of PA that can bind LF and BF, and heptamerize and form a pore in infected cells through which the toxin is delivered. The 63kD furin processed fragment of PA corresponds to amino

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acids 199-764 of the native full-length PA amino acid sequence of GenBank accession No. AAA2263 (SEQ ID NO:4) encoded by GenBank accession number M22589 (SEQ ID NO:3).

5 Figure 2 shows the nucleotide sequence (SEQ ID NO:5) and amino acid translation (SEQ ID NO:6) of TPA-PA63ΔF313-314. SEQ ID NO:5 is identical to SEQ ID NO:1, except that the nucleotides encoding the two phenylalanine residues at amino acids 313-314 of SEQ ID NO:2 are deleted, which results in a PA protein that cannot form the pore through which LF and EF are translocated. Nucleotides 1-12 of SEQ ID NO:5 is a Kozak translation
10 initiation element and nucleotides 13-81 of SEQ ID NO:5 encode the TPA signal peptide.

Figure 3 shows the nucleotide sequence (SEQ ID NO:7) and amino acid translation (SEQ ID NO:8) encoding TPA-PA83 Δ Furin. SEQ ID NO:7 contains a nucleic acid fragment of a human codon-optimized PA coding
15 region, encoding full-length mature PA (amino acids 30-764 of SEQ ID NO:4) with the furin cleavage site deleted (SRKKRS, amino acids 192-197 of SEQ ID NO:4). This mutant PA cannot be processed to the 63 kD fragment and cannot bind LF or EF. Nucleotides 1-12 of SEQ ID NO:7 is a Kozak translation initiation element and nucleotides 13-81 of SEQ ID NO:7 encode
20 the TPA signal peptide.

Figure 4 shows the nucleotide sequence (SEQ ID NO:9) and amino acid translation (SEQ ID NO:10) of TPA-LF HEXXH (H686A+H690A+E687D). SEQ ID NO:9 contains a nucleic acid fragment of a human codon-optimized LF coding region, encoding the mature *Bacillus anthracis* lethal factor with three inactivating point mutations. Either the
25 H686A + H690A (decreased Zn binding and no protease activity) or E687D (no protease activity, no *in vitro* or *in vivo* macrophage killing) mutation inactivates the enzymatic activity of LF rendering it non-toxic (Hammond S.E. and Hanna P.C. *Infect Immun.* 66:2374-2378(1998)). This construct
30 combines both sets of mutations. Nucleotides 1-12 of SEQ ID NO:9 is a Kozak translation initiation element and nucleotides 13-81 of SEQ ID NO:9

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encode the TPA signal peptide. Nucleotides 82- 2412 encode a non-toxic form of lethal factor. TPA-LF HEXXH (H686A+H690A+E687D) is derived from the native full-length LF amino acid sequence of GenBank accession No. AAA22569 (SEQ ID NO:12) encoded by GenBank accession number M30210 (SEQ ID NO:11).

Figure 5 shows the nucleotide sequence (SEQ ID NO:13) and amino acid translation (SEQ ID NO:14) of TPA-LF Domain I-III. SEQ ID NO:13 contains a nucleic acid fragment of a human codon-optimized LF coding region, encoding an N-terminal fragment (domains I-III) of LF corresponding to amino acids 34-583 of SEQ ID NO:12. Nucleotides 1-12 of SEQ ID NO:13 is a Kozak translation initiation element and nucleotides 13-81 of SEQ ID NO:13 encode the TPA signal peptide. Nucleotides 82-1734 of SEQ ID NO:13 encode domains I-III of LF. The entire protease domain (domain IV) has been deleted.

Figure 6 shows the nucleotide sequence (SEQ ID NO:15) and amino acid translation (SEQ ID NO:16) of TPA-LF Domain IA. SEQ ID NO:15 contains a nucleic acid fragment of a human codon-optimized LF coding region, encoding an LF N-terminal fragment of LF corresponding to amino acids 34-254 of SEQ ID NO:12. This truncated version of LF roughly corresponds to the domain I portion of LF that directly binds PA63. Pannifer A.D. *et al.* Nature 414:229-333 (2001). Nucleotides 1-12 of SEQ ID NO:15 is a Kozak translation initiation element and nucleotides 13-81 of SEQ ID NO:15 encode the TPA signal peptide. Nucleotides 82-747 of SEQ ID NO:15 encode domain I of LF.

Figure 7 shows the nucleotide sequence (SEQ ID NO:17) and amino acid translation (SEQ ID NO:18) of TPA-PA63 with the N-linked glycosylation motifs mutated. SEQ ID NO:17 is identical to SEQ ID NO:1, except that all ten N-linked glycosylation sites have been mutated. The N residue in the glycosylation motif (N-X-S/T) has been changed to a Q residue (Q-X-S/T) resulting in a protein that cannot glycosylated at these sites. Nucleotides 1-12 of SEQ ID NO:17 is a Kozak translation initiation element

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and nucleotides 13-81 of SEQ ID NO:17 encode the TPA signal peptide. Nucleotides 82-747 of SEQ ID NO:15 encode domain I of LF. Nucleotides 82-1782 of SEQ ID NO:17 encode a mutated form of the 63kD furin processed fragment of PA that can heptamerize, bind LF and EF, and form a pore in infected cells through which the toxin is delivered.

Figure 8 shows the nucleotide sequence (SEQ ID NO:19) and amino acid translation (SEQ ID NO:20) of sugar-minus TPA-LF HEXXH mutant (H686A+H690A+E687D). SEQ ID NO:19 is identical to SEQ ID NO:9, except that all seven N-linked glycosylation sites have been mutated. The N residue in the glycosylation motif (N-X-S/T) has been changed to a Q residue (Q-X-S/T) resulting in a protein that cannot be glycosylated at these sites. Nucleotides 1-12 of SEQ ID NO:19 is a Kozak translation initiation element and nucleotides 13-81 of SEQ ID NO:19 encode the TPA signal peptide. Nucleotides 82- 2412 encode a non-toxic form of lethal factor which cannot be glycosylated.

Figure 9 shows a nucleotide sequence comparison of a nucleic acid fragment of a human codon-optimized PA coding region, encoding PA63 (nucleotides 82-1782 of SEQ ID NO:1) vs. the native nucleotide sequence of *Bacillus anthracis* PA63 (nucleotides 2398-4095 of SEQ ID NO:3). Differences between the two sequences are denoted with a letter. There is approximately 25% difference in the two coding sequences.

Figure 10 shows a nucleotide sequence comparison of a humanized nucleotide sequence encoding the mature PA Δ furin (nucleotides 82-2268 of SEQ ID NO: 7) vs. the native nucleotide sequence of *Bacillus anthracis* mature PA (nucleotides 1891-4095 of SEQ ID NO:3). Differences between the two sequences are denoted with a letter and gaps are denoted as a dash. There is approximately 25% difference in the two coding sequences.

Figure 11 shows a nucleotide sequence comparison of a humanized nucleotide sequence encoding the mature LF Δ HEXXH (nucleotides 82-2409 of SEQ ID NO:9) vs. the native nucleotide sequence of *Bacillus anthracis* mature LF (nucleotides 784-3111 of SEQ ID NO:11). Differences between

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the two sequences are denoted with a letter and gaps are denoted by a gap. There is approximately 25% difference in the two coding sequences.

Figure 12 shows an amino acid comparison between TPA-PA63 (SEQ ID NO:2) and sugar minus TPA-PA63 (SEQ ID NO:18). All ten N-linked glycosylation sites N-X-S/T in TPA-PA63 have been mutated to Q-X-S/T so that they will not be a substrate for glycosylation.

Figure 13 shows an amino acid comparison between TPA-LFAHEXXH (SEQ ID NO:10) and sugar minus TPA-LFAHEXXH (SEQ ID NO:20). All seven N-linked glycosylation sites N-X-S/T in TPA-PA63 have been mutated to Q-X-S/T so that they will not be a substrate for glycosylation.

Figure 14 shows the nucleotide sequence (SEQ ID NO:39) and amino acid translation (SEQ ID NO:40) of TPA-LF Domain IB. SEQ ID NO:39 contains a nucleic acid fragment of a human codon-optimized LF coding region, encoding an LF N-terminal fragment of LF corresponding to amino acids 34-295 of SEQ ID NO:12. This truncated version of LF roughly corresponds to the domain I portion of LF that directly binds PA63. Pannifer A.D. *et al.* Nature 414:229-333 (2001). Nucleotides 1-12 of SEQ ID NO:39 is a Kozak translation initiation element and nucleotides 13-81 of SEQ ID NO:39 encode the TPA signal peptide. Nucleotides 82-870 of SEQ ID NO:39 encode domain I of LF.

Figure 15: Antibody titers measured in mouse immunization experiment 1 (Example 11). 15A: protective antigen (PA) titers; 15B: lethal factor (LF) titers; and 15C: lethal toxin (LT) neutralization titers.

Figure 16: Antibody titers measured in mouse immunization experiment 2 (Example 11). 16A: protective antigen (PA) titers; 16B: lethal factor (LF) titers; and 16C: lethal toxin (LT) neutralization titers.

Figure 17: Antibody titers measured in mouse immunization experiment 3 (Example 11). 17A: protective antigen (PA) titers; 17B: lethal factor (LF) titers; and 17C: lethal toxin (LT) neutralization titers.

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Figure 18: Antibody titers measured in mouse immunization experiment 4 (Example 11). 18A: protective antigen (PA) titers; 185B: lethal toxin (LT) neutralization titers.

5 Figure 19: Pre-challenge lethal toxin (LT) neutralization titers in the rabbit immunization experiment (Example 12).

Figure 20: Antibody titers measured in mouse immunization experiment 5 (Example 11).

Figure 21: Lethal toxin (LT) neutralization titers in mouse immunization experiment 5 (Example 11).

10

DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed to compositions and methods for enhancing the immune response of a vertebrate in need of protection against *Bacillus anthracis* infection by administering *in vivo*, into a tissue of a vertebrate, a polynucleotide comprising a human codon-optimized coding region encoding a polypeptide of *Bacillus anthracis*, or a nucleic acid
15 fragment of such a coding region encoding a fragment, variant, or derivative thereof. The polynucleotides are incorporated into the cells of the vertebrate *in vivo*, and an immunologically effective amount of the *Bacillus anthracis* polypeptide, or fragment or variant is produced *in vivo*.

20 The present invention provides polynucleotide-based vaccines and methods for delivery of *Bacillus anthracis* coding sequences to a vertebrate with optimal expression and safety conferred through codon optimization and/or other manipulations. These polynucleotide-based vaccines are prepared and administered in such a manner that the encoded gene products are
25 optimally expressed in the particular vertebrate to which the composition is administered. As a result, these compositions and methods are useful in stimulating an immune response against *Bacillus anthracis* infection as the coding sequence encodes a polypeptide which stimulates the immune system to respond to anthrax infection. Also included in the invention are expression

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systems, delivery systems, and codon-optimized *Bacillus anthracis* coding sequences.

A polynucleotide vaccine of the present invention is capable of eliciting, without more, an immune response in a vertebrate against *B. anthracis* when administered to that vertebrate. Such polynucleotides are referred to herein as polynucleotide vaccines.

It is to be noted that the term "a" or "an" entity refers to one or more of that entity; for example, "a polynucleotide," is understood to represent one or more polynucleotides. As such, the terms "a" (or "an"), "one or more," and "at least one" can be used interchangeably herein.

The terms "nucleic acid" or "nucleic acid fragment" refers to any one or more nucleic acid segments, e.g., DNA or RNA fragments, present in a polynucleotide or construct. While the terms "nucleic acid," as used herein, is meant to include any nucleic acid, the term "nucleic acid fragment" is used herein to specifically denote a fragment of a designed or synthetic codon-optimized coding region encoding a polypeptide, or fragment, variant, or derivative thereof, which has been optimized according to the codon usage of a given species. As used herein, a "coding region" is a portion of nucleic acid which consists of codons translated into amino acids. Although a "stop codon" (TAG, TGA, or TAA) is not translated into an amino acid, it may be considered to be part of a coding region, but any flanking sequences, for example promoters, ribosome binding sites, transcriptional terminators, and the like, are not part of a coding region. Two or more nucleic acids of the present invention can be present in a single polynucleotide construct, e.g., on a single plasmid, or in separate polynucleotide constructs, e.g., on separate plasmids. Furthermore, any nucleic acid or nucleic acid fragment may encode a single polypeptide, e.g., a single antigen, cytokine, or regulatory polypeptide, or may encode more than one polypeptide, e.g., a nucleic acid may encode two or more polypeptides. In addition, a nucleic acid may encode a regulatory element such as a promoter or a transcription terminator, or may

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encode a specialized element or motif of a polypeptide or protein, such as a secretory signal peptide or a functional domain.

The terms "fragment," "variant," "derivative" and "analog" when referring to *B. anthracis* polypeptides of the present invention include any polypeptides which retain at least some of the immunogenicity or antigenicity of the corresponding native polypeptide. Fragments of *B. anthracis* polypeptides of the present invention include proteolytic fragments, deletion fragments and in particular, fragments of *B. anthracis* polypeptides which exhibit reduced pathogenicity when delivered to an animal. Polypeptide fragments further include any portion of the polypeptide which comprises an antigenic or immunogenic epitope of the native polypeptide, including linear as well as three-dimensional epitopes. Variants of *B. anthracis* polypeptides of the present invention includes fragments as described above, and also polypeptides with altered amino acid sequences due to amino acid substitutions, deletions, or insertions. Variants may occur naturally, such as an allelic variant. By an "allelic variant" is intended alternate forms of a gene occupying a given locus on a chromosome of an organism. *Genes II*, Lewin, B., ed., John Wiley & Sons, New York (1985). Non-naturally occurring variants may be produced using art-known mutagenesis techniques. Variant polypeptides may comprise conservative or non-conservative amino acid substitutions, deletions or additions. Derivatives of *B. anthracis* polypeptides of the present invention, are polypeptides which have been altered so as to exhibit additional features not found on the native polypeptide. Examples include fusion proteins. An analog is another form of a *B. anthracis* polypeptide of the present invention. An example is a proprotein (e.g., *B. anthracis* PA83) which can be activated by cleavage of the proprotein to produce an active mature polypeptide (e.g., *B. anthracis* PA63).

The term "polynucleotide" is intended to encompass a singular nucleic acid or nucleic acid fragment as well as plural nucleic acids or nucleic acid fragments, and refers to an isolated molecule or construct, e.g., a virus genome (e.g., a non-infectious viral genome), messenger RNA (mRNA), plasmid DNA

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(pDNA), or derivatives of pDNA (*e.g.*, minicircles as described in (Darquet, A-M *et al.*, *Gene Therapy* 4:1341-1349 (1997)) comprising a polynucleotide. A nucleic acid may be provided in linear (*e.g.*, mRNA), circular (*e.g.*, plasmid), or branched form as well as double-stranded or single-stranded forms. A polynucleotide may comprise a conventional phosphodiester bond or a non-conventional bond (*e.g.*, an amide bond, such as found in peptide nucleic acids (PNA)).

The terms "infectious polynucleotide" or "infectious nucleic acid" are intended to encompass isolated viral polynucleotides and/or nucleic acids which are solely sufficient to mediate the synthesis of complete infectious virus particles upon uptake by permissive cells. "Isolated" means that the viral nucleic acid does not require pre-synthesized copies of any of the polypeptides it encodes, *e.g.*, viral replicases, in order to initiate its replication cycle.

The terms "non-infectious polynucleotide" or "non-infectious nucleic acid" as defined herein which cannot, without additional added materials, *e.g.*, polypeptides, mediate the synthesis of complete infectious virus particles upon uptake by permissive cells. An infectious polynucleotide or nucleic acid is not made "non-infectious" simply because it is taken up by a non-permissive cell. For example, an infectious viral polynucleotide from a virus with limited host range is infectious if it is capable of mediating the synthesis of complete infectious virus particles when taken up by cells derived from a permissive host (*i.e.*, a host permissive for the virus itself). The fact that uptake by cells derived from a non-permissive host does not result in the synthesis of complete infectious virus particles does not make the nucleic acid "non-infectious." In other words, the term is not qualified by the nature of the host cell, the tissue type, or the species.

In some cases, an isolated infectious polynucleotide or nucleic acid may produce fully-infectious virus particles in a host cell population which lacks receptors for the virus particles, *i.e.*, is non-permissive for the virus itself. Thus viruses produced will not infect surrounding cells. However, if

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the supernatant containing the virus particles is transferred to cells which are permissive for the virus, infection will take place.

The terms "replicating polynucleotide" or "replicating nucleic acid" are meant to encompass those polynucleotides and/or nucleic acids which, upon being taken up by a permissive host cell, are capable of producing multiple, *e.g.*, one or more copies of the same polynucleotide or nucleic acid. Infectious polynucleotides and nucleic acids are a subset of replicating polynucleotides and nucleic acids; the terms are not synonymous. For example, a defective virus genome lacking the genes for virus coat proteins may replicate, *e.g.*, produce multiple copies of itself, but is NOT infectious because it is incapable of mediating the synthesis of complete infectious virus particles unless the coat proteins, or another nucleic acid encoding the coat proteins, are provided.

In certain embodiments, the polynucleotide, nucleic acid, or nucleic acid fragment is DNA. In the case of DNA, a polynucleotide comprising a nucleic acid which encodes a polypeptide normally also comprises a promoter operably associated with the polypeptide-encoding nucleic acid. An operable association is when a nucleic acid encoding a gene product, *e.g.*, a polypeptide, is associated with one or more regulatory sequences in such a way as to place expression of the gene product under the influence or control of the regulatory sequence(s). Two DNA fragments (such as a polypeptide-encoding nucleic acid and a promoter associated with the 5' end of the nucleic acid) are "operably associated" if induction of promoter function results in the transcription of mRNA encoding the desired gene product and if the nature of the linkage between the two DNA fragments does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the expression regulatory sequences to direct the expression of the gene product, or (3) interfere with the ability of the DNA template to be transcribed. Thus, a promoter region would be operably associated with a nucleic acid encoding a polypeptide if the promoter was capable of effecting transcription of that nucleic acid. The promoter may be a cell-specific promoter that directs substantial transcription of the DNA only in predetermined cells. Other

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transcription control elements, besides a promoter, for example enhancers, operators, repressors, and transcription termination signals, can be operably associated with the polynucleotide to direct cell-specific transcription. Suitable promoters and other transcription control regions are disclosed herein.

5 A variety of transcription control regions are known to those skilled in the art. These include, without limitation, transcription control regions which function in vertebrate cells, such as, but not limited to, promoter and enhancer segments from cytomegaloviruses (the immediate early promoter, in conjunction with intron-A), simian virus 40 (the early promoter), retroviruses
10 (such as Rous sarcoma virus), and picornaviruses (particularly an internal ribosome entry site, or IRES, also referred to as a CITE sequence). Other transcription control regions include those derived from vertebrate genes such as actin, heat shock protein, bovine growth hormone and rabbit β -globin, as well as other sequences capable of controlling gene expression in eukaryotic
15 cells. Additional suitable transcription control regions include tissue-specific promoters and enhancers as well as lymphokine-inducible promoters (*e.g.*, promoters inducible by interferons or interleukins).

In one embodiment, a DNA polynucleotide of the present invention is a circular or linearized plasmid, or other linear DNA which is, in certain
20 embodiments, non-infectious and nonintegrating (*i.e.*, does not integrate into the genome of vertebrate cells). A linearized plasmid is a plasmid that was previously circular but has been linearized, for example, by digestion with a restriction endonuclease.

Alternatively, DNA virus genomes may be used to administer DNA
25 polynucleotides into vertebrate cells. In certain embodiments, a DNA virus genome of the present invention is noninfectious, and nonintegrating. Suitable DNA virus genomes include herpesvirus genomes, adenovirus genomes, adeno-associated virus genomes, and poxvirus genomes. References citing methods for the *in vivo* introduction of non-infectious virus genomes to
30 vertebrate tissues are well known to those of ordinary skill in the art, and are cited *supra*.

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In other embodiments, a polynucleotide of the present invention is RNA. In a suitable embodiment, the RNA is in the form of messenger RNA (mRNA). Methods for introducing RNA sequences into vertebrate cells are described in U.S. Patent No. 5,580,859, the disclosure of which is
5 incorporated herein by reference in its entirety.

Polynucleotide, nucleic acids, and nucleic acid fragments of the present invention may be associated with additional nucleic acids which encode secretory or signal peptides, which direct the secretion of a polypeptide encoded by a nucleic acid or polynucleotide of the present
10 invention. According to the signal hypothesis, proteins secreted by mammalian cells have a signal peptide or secretory leader sequence which is cleaved from the mature protein once export of the growing protein chain across the rough endoplasmic reticulum has been initiated. Those of ordinary skill in the art are aware that polypeptides secreted by vertebrate cells
15 generally have a signal peptide fused to the N-terminus of the polypeptide, which is cleaved from the complete or "full length" polypeptide to produce a secreted or "mature" form of the polypeptide. In certain embodiments, the native leader sequence is used, or a functional derivative of that sequence that retains the ability to direct the secretion of the polypeptide that is operably
20 associated with it. Alternatively, a heterologous mammalian leader sequence, or a functional derivative thereof, may be used. For example, the wild-type leader sequence may be substituted with the leader sequence of human tissue plasminogen activator (TPA) or mouse β -glucuronidase.

In accordance with one aspect of the present invention, there is
25 provided a plasmid for expression of a *Bacillus anthracis* PA or LF-derived coding sequence optimized for expression in the particular vertebrate species to be treated or immunized. When such a plasmid is delivered, *in vivo* to a tissue of the vertebrate to be treated or immunized, the transcriptional unit will thus express the encoded gene product. The level of expression of the gene
30 product will depend to a significant extent on the strength of the associated

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promoter and the presence and activation of an associated enhancer element, as well as the optimization of the coding region.

As used herein, the term "plasmid" refers to a construct made up of genetic material (*i.e.*, nucleic acids). Typically a plasmid contains an origin of replication which is functional in bacterial host cells, *e.g.*, *Escherichia coli*, and selectable markers for detecting bacterial host cells comprising the plasmid. Plasmids of the present invention may include genetic elements as described herein arranged such that an inserted coding sequence can be transcribed in eukaryotic cells. Also, while the plasmid may include a sequence from a viral nucleic acid, such viral sequence normally does not cause the incorporation of the plasmid into a viral particle, and the plasmid is therefore a non-viral vector. In certain embodiments described herein, a plasmid is a closed circular DNA molecule.

The term "expression" refers to the biological production of a product encoded by a coding sequence. In most cases a DNA sequence, including the coding sequence, is transcribed to form a messenger-RNA (mRNA). The messenger-RNA is translated to form a polypeptide product which has a relevant biological activity. Also, the process of expression may involve further processing steps to the RNA product of transcription, such as splicing to remove introns, and/or post-translational processing of a polypeptide product.

As used herein, the term "polypeptide" is intended to encompass a singular "polypeptide" as well as plural "polypeptides," and comprises any chain or chains of two or more amino acids. Thus, as used herein, terms including, but not limited to "peptide," "dipeptide," "tripeptide," "protein," "amino acid chain," or any other term used to refer to a chain or chains of two or more amino acids, are included in the definition of a "polypeptide," and the term "polypeptide" may be used instead of, or interchangeably with any of these terms. The term further includes polypeptides which have undergone post-translational modifications, for example, glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking

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groups, proteolytic cleavage, or modification by non-naturally occurring amino acids.

Also included as polypeptides of the present invention are fragments, derivatives, analogs, or variants of the foregoing polypeptides, and any combination thereof. Polypeptides, and fragments, derivatives, analogs, or variants thereof of the present invention can be antigenic and immunogenic polypeptides related to *B. anthracis* polypeptides, which are used to prevent or treat, *i.e.*, cure, ameliorate, lessen the severity of, or prevent or reduce contagion of infectious disease caused by *B. anthracis*.

As used herein, an antigenic polypeptide or an immunogenic polypeptide is a polypeptide which, when introduced into a vertebrate, reacts with the immune system molecules of the vertebrate, *i.e.*, is antigenic, and/or induces an immune response in the vertebrate, *i.e.*, is immunogenic. It is quite likely that an immunogenic polypeptide will also be antigenic, but an antigenic polypeptide, because of its size or conformation, may not necessarily be immunogenic. Examples of antigenic and immunogenic polypeptides of the present invention include, but are not limited to, *B. anthracis* protective antigen (PA) or lethal factor (LF), fragments thereof, *e.g.*, PA63, LF domains I-III or domain I, variants thereof, *e.g.*, PA63Δ FF, PA83 Δ furin, PA63 sugar minus, LF HEXXH, or LF sugar minus (all described in more detail herein) and derivatives thereof, *e.g.*, any of the foregoing polypeptides fused to a TPA signal peptide.

The term "epitopes," as used herein, refers to portions of a polypeptide having antigenic or immunogenic activity in an animal, for example a mammal, for example, a human. An "immunogenic epitope," as used herein, is defined as a portion of a protein that elicits an immune response in an animal, as determined by any method known in the art. The term "antigenic epitope," as used herein, is defined as a portion of a protein to which an antibody can immunospecifically bind its antigen as determined by any method well known in the art. Immunospecific binding excludes non-specific binding but does not

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necessarily exclude cross-reactivity with other antigens. Antigenic epitopes need not necessarily be immunogenic.

In the present invention, antigenic epitopes preferably contain a sequence of at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, or between about 15 to about 30 amino acids contained within the amino acid sequence of a polypeptide of the invention. Certain polypeptides comprising immunogenic or antigenic epitopes are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 amino acid residues in length. Antigenic as well as immunogenic epitopes may be linear, *i.e.*, be comprised of contiguous amino acids in a polypeptide, or may be three dimensional, *i.e.*, where an epitope is comprised of non-contiguous amino acids which come together due to the secondary or tertiary structure of the polypeptide, thereby forming an epitope.

The present invention is directed towards polynucleotides comprising nucleic acid fragments of codon-optimized coding regions which encode polypeptides of *Bacillus anthracis*, and in particular, *Bacillus anthracis* protective antigen (PA) or lethal factor (LF), and fragments, variants, or derivatives thereof.

"Codon optimization" is defined as modifying a nucleic acid sequence for enhanced expression in the cells of the vertebrate of interest by replacing at least one, more than one, or a significant number, of codons of the native sequence with codons that are more frequently or most frequently used in the genes of that vertebrate. Various species exhibit particular bias for certain codons of a particular amino acid.

The present invention relates to polynucleotides comprising nucleic acid fragments of codon-optimized coding regions which encode *Bacillus anthracis* polypeptides, with the codon usage adapted for optimized expression in the cells of a given vertebrate. These polynucleotides are prepared by incorporating codons preferred for use in the genes of a given species into the DNA sequence. Also provided are polynucleotide expression constructs, vectors, host cells comprising nucleic acid fragments of codon-

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optimized coding regions which encode *Bacillus anthracis* polypeptides, and various methods of using the polynucleotide expression constructs, vectors, host cells to treat or prevent anthrax in a vertebrate.

5 Codon Optimization

As used herein the term "codon optimized coding region" means a nucleic acid coding region that has been adapted for expression in the cells of a given vertebrate by replacing at least one, or more than one, or a significant number, of codons with one or more codons that are more frequently used in the genes of that vertebrate.

Deviations in the nucleotide sequence that comprise the codons encoding the amino acids of any polypeptide chain allow for variations in the sequence coding for the gene. Since each codon consists of three nucleotides, and the nucleotides comprising DNA are restricted to four specific bases, there are 64 possible combinations of nucleotides, 61 of which encode amino acids (the remaining three codons encode signals ending translation). The "genetic code" which shows which codons encode which amino acids is reproduced herein as Table 1. As a result, many amino acids are designated by more than one codon. For example, the amino acids alanine and proline are coded for by four triplets, serine and arginine by six, whereas tryptophan and methionine are coded by just one triplet. This degeneracy allows for DNA base composition to vary over a wide range without altering the amino acid sequence of the proteins encoded by the DNA.

TABLE 1: The Standard Genetic Code

	T	C	A	G
T	TTT Phe (F) TTC " TTA Leu (L) TTG "	TCT Ser (S) TCC " TCA " TCG "	TAT Tyr (Y) TAC " TAA Ter TAG Ter	TGT Cys (C) TGC TGA Ter TGG Trp (W)
C	CTT Leu (L) CTC " CTA " CTG "	CCT Pro (P) CCC " CCA " CCG "	CAT His (H) CAC " CAA Gln (Q) CAG "	CGT Arg (R) CGC " CGA " CGG "
A	ATT Ile (I) ATC " ATA " ATG Met (M)	ACT Thr (T) ACC " ACA " ACG "	AAT Asn (N) AAC " AAA Lys (K) AAG "	AGT Ser (S) AGC " AGA Arg (R) AGG "
G	GTT Val (V) GTC " GTA " GTG "	GCT Ala (A) GCC " GCA " GCG "	GAT Asp (D) GAC " GAA Glu (E) GAG "	GGT Gly (G) GGC " GGA " GGG "

5 Many organisms display a bias for use of particular codons to code for
insertion of a particular amino acid in a growing peptide chain. Codon
preference or codon bias, differences in codon usage between organisms, is
afforded by degeneracy of the genetic code, and is well documented among
many organisms. Codon bias often correlates with the efficiency of translation
10 of messenger RNA (mRNA), which is in turn believed to be dependent on,
inter alia, the properties of the codons being translated and the availability of
particular transfer RNA (tRNA) molecules. The predominance of selected
tRNAs in a cell is generally a reflection of the codons used most frequently in
peptide synthesis. Accordingly, genes can be tailored for optimal gene
15 expression in a given organism based on codon optimization.

Given the large number of gene sequences available for a wide variety
of animal, plant and microbial species, it is possible to calculate the relative

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frequencies of codon usage. Codon usage tables are readily available, for example, at the "Codon Usage Database" available at <http://www.kazusa.or.jp/codon/> (visited July 9, 2002), and these tables can be adapted in a number of ways. See Nakamura, Y., *et al.* "Codon usage tabulated from the international DNA sequence databases: status for the year 2000" *Nucl. Acids Res.* 28:292 (2000). Codon usage tables for human, mouse, domestic cat, and cow, calculated from GenBank Release 128.0 [15 February 2002], are reproduced below as Tables 2-5. These tables use mRNA nomenclature, and so instead of thymine (T) which is found in DNA, the tables use uracil (U) which is found in RNA. The tables have been adapted so that frequencies are calculated for each amino acid, rather than for all 64 codons.

TABLE 2: Codon Usage Table for Human Genes (*Homo sapiens*)

Amino Acid	Codon	Number	Frequency
Phe	UUU	326146	0.4525
Phe	UUC	394680	0.5475
Total		720826	
Leu	UUA	139249	0.0728
Leu	UUG	242151	0.1266
Leu	CUU	246206	0.1287
Leu	CUC	374262	0.1956
Leu	CUA	133980	0.0700
Leu	CUG	777077	0.4062
Total		1912925	
Ile	AUU	303721	0.3554
Ile	AUC	414483	0.4850
Ile	AUA	136399	0.1596
Total		854603	
Met	AUG	430946	1.0000
Total		430946	
Val	GUU	210423	0.1773
Val	GUC	282445	0.2380
Val	GUA	134991	0.1137

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Amino Acid	Codon	Number	Frequency
Val	GUG	559044	0.4710
Total		1186903	
Ser	UCU	282407	0.1840
Ser	UCC	336349	0.2191
Ser	UCA	225963	0.1472
Ser	UCG	86761	0.0565
Ser	AGU	230047	0.1499
Ser	AGC	373362	0.2433
Total		1534889	
Pro	CCU	333705	0.2834
Pro	CCC	386462	0.3281
Pro	CCA	322220	0.2736
Pro	CCG	135317	0.1149
Total		1177704	
Thr	ACU	247913	0.2419
Thr	ACC	371420	0.3624
Thr	ACA	285655	0.2787
Thr	ACG	120022	0.1171
Total		1025010	
Ala	GCU	360146	0.2637
Ala	GCC	551452	0.4037
Ala	GCA	308034	0.2255
Ala	GCG	146233	0.1071
Total		1365865	
Tyr	UAU	232240	0.4347
Tyr	UAC	301978	0.5653
Total		534218	
His	CAU	201389	0.4113
His	CAC	288200	0.5887
Total		489589	
Gln	CAA	227742	0.2541
Gln	CAG	668391	0.7459
Total		896133	

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Amino Acid	Codon	Number	Frequency
Asn	AAU	322271	0.4614
Asn	AAC	376210	0.5386
Total		698481	
Lys	AAA	462660	0.4212
Lys	AAG	635755	0.5788
Total		1098415	
Asp	GAU	430744	0.4613
Asp	GAC	502940	0.5387
Total		933684	
Glu	GAA	561277	0.4161
Glu	GAG	787712	0.5839
Total		1348989	
Cys	UGU	190962	0.4468
Cys	UGC	236400	0.5532
Total		427362	
Trp	UGG	248083	1.0000
Total		248083	
Arg	CGU	90899	0.0830
Arg	CGC	210931	0.1927
Arg	CGA	122555	0.1120
Arg	CGG	228970	0.2092
Arg	AGA	221221	0.2021
Arg	AGG	220119	0.2011
Total		1094695	
Gly	GGU	209450	0.1632
Gly	GGC	441320	0.3438
Gly	GGA	315726	0.2459
Gly	GGG	317263	0.2471
Total		1283759	
Stop	UAA	13963	
Stop	UAG	10631	
Stop	UGA	24607	

TABLE 3: Codon Usage Table for Mouse Genes (*Mus musculus*)

Amino Acid	Codon	Number	Frequency
Phe	UUU	150467	0.4321
Phe	UUC	197795	0.5679
Total		348262	
Leu	UUA	55635	0.0625
Leu	UUG	116210	0.1306
Leu	CUU	114699	0.1289
Leu	CUC	179248	0.2015
Leu	CUA	69237	0.0778
Leu	CUG	354743	0.3987
Total		889772	
Ile	AUU	137513	0.3367
Ile	AUC	208533	0.5106
Ile	AUA	62349	0.1527
Total		408395	
Met	AUG	204546	1.0000
Total		204546	
Val	GUU	93754	0.1673
Val	GUC	140762	0.2513
Val	GUA	64417	0.1150
Val	GUG	261308	0.4664
Total		560241	
Ser	UCU	139576	0.1936
Ser	UCC	160313	0.2224
Ser	UCA	100524	0.1394
Ser	UCG	38632	0.0536
Ser	AGU	108413	0.1504
Ser	AGC	173518	0.2407
Total		720976	
Pro	CCU	162613	0.3036
Pro	CCC	164796	0.3077
Pro	CCA	151091	0.2821
Pro	CCG	57032	0.1065
Total		535532	

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Amino Acid	Codon	Number	Frequency
Thr	ACU	119832	0.2472
Thr	ACC	172415	0.3556
Thr	ACA	140420	0.2896
Thr	ACG	52142	0.1076
Total		484809	
Ala	GCU	178593	0.2905
Ala	GCC	236018	0.3839
Ala	GCA	139697	0.2272
Ala	GCG	60444	0.0983
Total		614752	
Tyr	UAU	108556	0.4219
Tyr	UAC	148772	0.5781
Total		257328	
His	CAU	88786	0.3973
His	CAC	134705	0.6027
Total		223491	
Gln	CAA	101783	0.2520
Gln	CAG	302064	0.7480
Total		403847	
Asn	AAU	138868	0.4254
Asn	AAC	187541	0.5746
Total		326409	
Lys	AAA	188707	0.3839
Lys	AAG	302799	0.6161
Total		491506	
Asp	GAU	189372	0.4414
Asp	GAC	239670	0.5586
Total		429042	
Glu	GAA	235842	0.4015
Glu	GAG	351582	0.5985
Total		587424	
Cys	UGU	97385	0.4716
Cys	UGC	109130	0.5284
Total		206515	

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Amino Acid	Codon	Number	Frequency
Trp	UGG	112588	1.0000
Total		112588	
Arg	CGU	41703	0.0863
Arg	CGC	86351	0.1787
Arg	CGA	58928	0.1220
Arg	CGG	92277	0.1910
Arg	AGA	101029	0.2091
Arg	AGG	102859	0.2129
Total		483147	
Gly	GGU	103673	0.1750
Gly	GGC	198604	0.3352
Gly	GGA	151497	0.2557
Gly	GGG	138700	0.2341
Total		592474	
Stop	UAA	5499	
Stop	UAG	4661	
Stop	UGA	10356	

TABLE 4: Codon Usage Table for Domestic Cat Genes (*Felis catus*)

Amino Acid	Codon	Number	Frequency of usage
Phe	UUU	1204.00	0.4039
Phe	UUC	1777.00	0.5961
Total		2981	
Leu	UUA	404.00	0.0570
Leu	UUG	857.00	0.1209
Leu	CUU	791.00	0.1116
Leu	CUC	1513.00	0.2135
Leu	CUA	488.00	0.0688
Leu	CUG	3035.00	0.4282
Total		7088	
Ile	AUU	1018.00	0.2984
Ile	AUC	1835.00	0.5380
Ile	AUA	558.00	0.1636
Total		3411	

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Amino Acid	Codon	Number	Frequency of usage
Met	AUG	1553.00	0.0036
Total		1553	
Val	GUU	696.00	0.1512
Val	GUC	1279.00	0.2779
Val	GUA	463.00	0.1006
Val	GUG	2164.00	0.4702
Total		4602	
Ser	UCU	940.00	0.1875
Ser	UCC	1260.00	0.2513
Ser	UCA	608.00	0.1213
Ser	UCG	332.00	0.0662
Ser	AGU	672.00	0.1340
Ser	AGC	1202.00	0.2397
Total		5014	
Pro	CCU	958.00	0.2626
Pro	CCC	1375.00	0.3769
Pro	CCA	850.00	0.2330
Pro	CCG	465.00	0.1275
Total		3648	
Thr	ACU	822.00	0.2127
Thr	ACC	1574.00	0.4072
Thr	ACA	903.00	0.2336
Thr	ACG	566.00	0.1464
Total		3865	
Ala	GCU	1129.00	0.2496
Ala	GCC	1951.00	0.4313
Ala	GCA	883.00	0.1952
Ala	GCG	561.00	0.1240
Total		4524	
Tyr	UAU	837.00	0.3779
Tyr	UAC	1378.00	0.6221
Total		2215	
His	CAU	594.00	0.3738
His	CAC	995.00	0.6262
Total		1589	

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Amino Acid	Codon	Number	Frequency of usage
Gln	CAA	747.00	0.2783
Gln	CAG	1937.00	0.7217
Total		2684	
Asn	AAU	1109.00	0.3949
Asn	AAC	1699.00	0.6051
Total		2808	
Lys	AAA	1445.00	0.4088
Lys	AAG	2090.00	0.5912
Total		3535	
Asp	GAU	1255.00	0.4055
Asp	GAC	1840.00	0.5945
Total		3095	
Glu	GAA	1637.00	0.4164
Glu	GAG	2294.00	0.5836
Total		3931	
Cys	UGU	719.00	0.4425
Cys	UGC	906.00	0.5575
Total		1625	
Trp	UGG	1073.00	1.0000
Total		1073	
Arg	CGU	236.00	0.0700
Arg	CGC	629.00	0.1865
Arg	CGA	354.00	0.1050
Arg	CGG	662.00	0.1963
Arg	AGA	712.00	0.2112
Arg	AGG	779.00	0.2310
Total		3372	
Gly	GGU	648.00	0.1498
Gly	GGC	1536.00	0.3551
Gly	GGA	1065.00	0.2462
Gly	GGG	1077.00	0.2490
Total		4326	

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Amino Acid	Codon	Number	Frequency of usage
Stop	UAA	55	
Stop	UAG	36	
Stop	UGA	110	

TABLE 5: Codon Usage Table for Cow Genes (*Bos taurus*)

Amino Acid	Codon	Number	Frequency of usage
Phe	UUU	13002	0.4112
Phe	UUC	18614	0.5888
Total		31616	
Leu	UUA	4467	0.0590
Leu	UUG	9024	0.1192
Leu	CUU	9069	0.1198
Leu	CUC	16003	0.2114
Leu	CUA	4608	0.0609
Leu	CUG	32536	0.4298
Total		75707	
Ile	AUU	12474	0.3313
Ile	AUC	19800	0.5258
Ile	AUA	5381	0.1429
Total		37655	
Met	AUG	17770	1.0000
Total		17770	
Val	GUU	8212	0.1635
Val	GUC	12846	0.2558
Val	GUA	4932	0.0982
Val	GUG	24222	0.4824
Total		50212	
Ser	UCU	10287	0.1804
Ser	UCC	13258	0.2325
Ser	UCA	7678	0.1347
Ser	UCG	3470	0.0609
Ser	AGU	8040	0.1410
Ser	AGC	14279	0.2505
Total		57012	

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Amino Acid	Codon	Number	Frequency of usage
Pro	CCU	11695	0.2684
Pro	CCC	15221	0.3493
Pro	CCA	11039	0.2533
Pro	CCG	5621	0.1290
Total		43576	
Thr	ACU	9372	0.2203
Thr	ACC	16574	0.3895
Thr	ACA	10892	0.2560
Thr	ACG	5712	0.1342
Total		42550	
Ala	GCU	13923	0.2592
Ala	GCC	23073	0.4295
Ala	GCA	10704	0.1992
Ala	GCG	6025	0.1121
Total		53725	
Tyr	UAU	9441	0.3882
Tyr	UAC	14882	0.6118
Total		24323	
His	CAU	6528	0.3649
His	CAC	11363	0.6351
Total		17891	
Gln	CAA	8060	0.2430
Gln	CAG	25108	0.7570
Total		33168	
Asn	AAU	12491	0.4088
Asn	AAC	18063	0.5912
Total		30554	
Lys	AAA	17244	0.3897
Lys	AAG	27000	0.6103
Total		44244	
Asp	GAU	16615	0.4239
Asp	GAC	22580	0.5761
Total		39195	

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Amino Acid	Codon	Number	Frequency of usage
Glu	GAA	21102	0.4007
Glu	GAG	31555	0.5993
Total		52657	
Cys	UGU	7556	0.4200
Cys	UGC	10436	0.5800
Total		17992	
Trp	UGG	10706	1.0000
Total		10706	
Arg	CGU	3391	0.0824
Arg	CGC	7998	0.1943
Arg	CGA	4558	0.1108
Arg	CGG	8300	0.2017
Arg	AGA	8237	0.2001
Arg	AGG	8671	0.2107
Total		41155	
Gly	GGU	8508	0.1616
Gly	GGC	18517	0.3518
Gly	GGA	12838	0.2439
Gly	GGG	12772	0.2427
Total		52635	
Stop	UAA	555	
Stop	UAG	394	
Stop	UGA	392	

By utilizing these or similar tables, one of ordinary skill in the art can apply the frequencies to any given polypeptide sequence, and produce a nucleic acid fragment of a codon-optimized coding region which encodes the polypeptide, but which uses codons optimal for a given species. Codon-optimized coding regions can be designed by various different methods.

In one method, a codon usage table is used to find the single most frequent codon used for any given amino acid, and that codon is used each time that particular amino acid appears in the polypeptide sequence. For example, referring to Table 2 above, for leucine, the most frequent codon is

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CUG, which is used 41% of the time. Thus all the leucine residues in a given amino acid sequence would be assigned the codon CUG. Human codon-optimized nucleotide sequences encoding native PA (GenBank Accession Number AAA2263 (SEQ ID NO:4)) and native LF (GenBank Accession Number AAA22569 (SEQ ID NO:12)) which have been optimized using this method are presented herein as SEQ ID NO:21 and SEQ ID NO:22, respectively.

In another method, the actual frequencies of the codons are distributed randomly throughout the coding sequence. Thus using this method for optimization, if a hypothetical polypeptide sequence had 100 leucine residues, referring to Table 2 for frequency of usage in the humans, about 7, or 7% of the leucine codons would be UUA, about 13, or 13% of the leucine codons would be UUG, about 13, or 13% of the leucine codons would be CUU, about 20, or 20% of the leucine codons would be CUC, about 7, or 7% of the leucine codons would be CUA, and about 41, or 41% of the leucine codons would be CUG. These frequencies would be distributed randomly throughout the leucine codons in the coding region encoding the hypothetical polypeptide. As will be understood by those of ordinary skill in the art, the distribution of codons in the sequence will can vary significantly using this method, however, the sequence always encodes the same polypeptide. Three different human codon-optimized nucleotide sequences encoding native PA (GenBank Accession Number AAA2263 (SEQ ID NO:4)) which have been optimized using this method are presented herein as SEQ ID NO:23, SEQ ID NO:24, and SEQ ID NO:25. Three different human codon-optimized sequences encoding native LF (GenBank Accession Number AAA22569 (SEQ ID NO:12)) which have been optimized using this method are presented herein as SEQ ID NO:21 and SEQ ID NO:22, respectively.

When using the latter method, the term "about" is used precisely to account for fractional percentages of codon frequencies for a given amino acid. As used herein, "about" is defined as one amino acid more or one amino acid less than the value given. The whole number value of amino acids is

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rounded up if the fractional frequency of usage is 0.50 or greater, and is rounded down if the fractional frequency of use is 0.49 or less. Using again the example of the frequency of usage of leucine in human genes for a hypothetical polypeptide having 62 leucine residues, the fractional frequency of codon usage would be calculated by multiplying 62 by the frequencies for the various codons. Thus, 7.28 percent of 62 equals 4.51 UUA codons, or "about 5," *i.e.*, 4, 5, or 6 UUA codons, 12.66 percent of 62 equals 7.85 UUG codons or "about 8," *i.e.*, 7, 8, or 9 UUG codons, 12.87 percent of 62 equals 7.98 CUU codons, or "about 8," *i.e.*, 7, 8, or 9 CUU codons, 19.56 percent of 62 equals 12.13 CUC codons or "about 12," *i.e.*, 11, 12, or 13 CUC codons, 7.00 percent of 62 equals 4.34 CUA codons or "about 4," *i.e.*, 3, 4, or 5 CUA codons, and 40.62 percent of 62 equals 25.19 CUG codons, or "about 25," *i.e.*, 24, 25, or 26 CUG codons.

Randomly assigning codons at an optimized frequency to encode a given polypeptide sequence, can be done manually by calculating codon frequencies for each amino acid, and then assigning the codons to the polypeptide sequence randomly. Additionally, various algorithms and computer software programs are readily available to those of ordinary skill in the art. For example, the "EditSeq" function in the Lasergene Package, available from DNASTar, Inc., Madison, WI, the backtranslation function in the VectorNTI Suite, available from InformMax, Inc., Bethesda, MD, and the "backtranslate" function in the GCG--Wisconsin Package, available from Accelrys, Inc., San Diego, CA. In addition, various resources are publicly available to codon-optimize coding region sequences. For example, the "backtranslation" function at <http://www.entelechon.com/eng/backtranslation.html> (visited July 9, 2002), the "backtranseq" function available at <http://bioinfo.pbi.nrc.ca:8090/EMBOSS/index.html> (visited July 9, 2002). Constructing a rudimentary algorithm to assign codons based on a given frequency can also easily be accomplished with basic mathematical functions by one of ordinary skill.

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A number of options are available for synthesizing codon optimized coding regions designed by any of the methods described above, using standard and routine molecular biological manipulations well known to those of ordinary skill in the art. In one approach, a series of complementary oligonucleotide pairs of 80-90 nucleotides each in length and spanning the length of the desired sequence are synthesized by standard methods. These oligonucleotide pairs are synthesized such that upon annealing, they form double stranded fragments of 80-90 base pairs, containing cohesive ends, *e.g.*, each oligonucleotide in the pair is synthesized to extend 3, 4, 5, 6, 7, 8, 9, 10, or more bases beyond the region that is complementary to the other oligonucleotide in the pair. The single-stranded ends of each pair of oligonucleotides is designed to anneal with the single-stranded end of another pair of oligonucleotides. The oligonucleotide pairs are allowed to anneal, and approximately five to six of these double-stranded fragments are then allowed to anneal together via the cohesive single stranded ends, and then they ligated together and cloned into a standard bacterial cloning vector, for example, a TOPO® vector available from Invitrogen Corporation, Carlsbad, CA. The construct is then sequenced by standard methods. Several of these constructs consisting of 5 to 6 fragments of 80 to 90 base pair fragments ligated together, *i.e.*, fragments of about 500 base pairs, are prepared, such that the entire desired sequence is represented in a series of plasmid constructs. The inserts of these plasmids are then cut with appropriate restriction enzymes and ligated together to form the final construct. The final construct is then cloned into a standard bacterial cloning vector, and sequenced. Additional methods would be immediately apparent to the skilled artisan. In addition, gene synthesis is readily available commercially.

In certain embodiments, an entire polypeptide sequence, or fragment, variant, or derivative thereof is codon optimized by any of the methods described herein. Various desired fragments, variants or derivatives are designed, and each is then codon-optimized individually. In addition, partially codon-optimized coding regions of the present invention can be designed and

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constructed. For example, the invention includes a nucleic acid fragment of a codon-optimized coding region encoding a polypeptide in which at least about 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of the codon positions have been codon-optimized for a given species. That is, they contain a codon that is preferentially used in the genes of a desired species, e.g., a vertebrate species, e.g., humans, in place of a codon that is normally used in the native nucleic acid sequence.

In additional embodiments, a full-length polypeptide sequence is codon-optimized for a given species resulting in a codon-optimized coding region encoding the entire polypeptide, and then nucleic acid fragments of the codon-optimized coding region, which encode fragments, variants, and derivatives of the polypeptide are made from the original codon-optimized coding region. As would be well understood by those of ordinary skill in the art, if codons have been randomly assigned to the full-length coding region based on their frequency of use in a given species, nucleic acid fragments encoding fragments, variants, and derivatives would not necessarily be *fully* codon optimized for the given species. However, such sequences are still much closer to the codon usage of the desired species than the native codon usage. The advantage of this approach is that synthesizing codon-optimized nucleic acid fragments encoding each fragment, variant, and derivative of a given polypeptide, although routine, would be time consuming and would result in significant expense.

The codon-optimized coding regions can be versions encoding any gene products from any strain of *Bacillus anthracis*, or fragments, variants, or derivatives of such gene products. Described herein are nucleic acid fragments of codon-optimized coding regions encoding the *Bacillus anthracis* protective antigen (PA) gene and the *Bacillus anthracis* lethal factor (LF), the nucleic acid fragments encoding the complete polypeptide, as well as various fragments, variants, and derivatives thereof, although other PA or LF - encoding nucleic acid sources are not excluded.

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The present invention is directed to compositions and methods of enhancing the immune response of a vertebrate in need of protection against *Bacillus anthracis* infection by administering *in vivo*, into a tissue of a vertebrate, a polynucleotide comprising a codon-optimized coding region encoding a polypeptide of *Bacillus anthracis*, or a nucleic acid fragment of such a coding region encoding a fragment, variant or derivative thereof. Codon optimization is carried out for a particular vertebrate species by methods described herein, for example, in certain embodiments codon-optimized coding regions encoding polypeptides of *Bacillus anthracis*, or nucleic acid fragments of such coding regions encoding fragments, variants, or derivatives thereof are optimized according to human codon usage. The polynucleotides of the invention are incorporated into the cells of the vertebrate *in vivo*, and an immunologically effective amount of a *Bacillus anthracis* polypeptide is produced *in vivo*. In particular, the present invention relates to codon-optimized coding regions encoding polypeptides of *Bacillus anthracis*, or nucleic acid fragments of such coding regions fragments, variants, or derivatives thereof which have been optimized according to mammalian codon usage, for example, human codon usage, cow codon usage, domestic cat codon usage, or mouse codon usage. For example, human codon-optimized coding regions encoding polypeptides of *Bacillus anthracis*, or nucleic acid fragments of such coding regions encoding fragments, variants, or derivatives thereof are prepared by incorporating codons preferred for use in human genes into the DNA sequence encoding the *B. anthracis* polypeptide. Also provided are polynucleotides, vectors, and other expression constructs comprising codon-optimized coding regions encoding polypeptides of *Bacillus anthracis*, or nucleic acid fragments of such coding regions encoding fragments, variants, or derivatives thereof, and various methods of using such polynucleotides, vectors and other expression constructs.

The present invention is further directed towards polynucleotides comprising codon-optimized coding regions encoding polypeptides of *Bacillus anthracis* toxin, for example, *Bacillus anthracis* lethal toxin and its

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component polypeptides, for example, lethal factor (LF) and protective antigen (PA). The invention is also directed to polynucleotides comprising codon-optimized nucleic acid fragments encoding fragments, variants and derivatives of these polypeptides.

The present invention provides isolated polynucleotides comprising codon-optimized coding regions of *Bacillus anthracis* PA, or fragments, variants, or derivatives thereof. In certain embodiments described herein, a codon-optimized coding region encoding SEQ ID NO:4 is optimized according to codon usage in humans (*Homo sapiens*). Alternatively, a codon-optimized coding region encoding SEQ ID NO:4 may be optimized according to codon usage in any plant, animal, or microbial species.

Codon-optimized coding regions encoding SEQ ID NO:4, optimized according to codon usage in humans are designed as follows. The amino acid composition of SEQ ID NO:4 is shown in Table 6.

TABLE 6

Amino Acid		Number in SEQ ID NO:4
A	Ala	41
R	Arg	29
C	Cys	0
G	Gly	36
H	His	10
I	Ile	57
L	Leu	62
K	Lys	60
M	Met	10
F	Phe	24
P	Pro	29
S	Ser	72
T	Thr	58
W	Trp	7
Y	Tyr	28
V	Val	43
N	Asn	69

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D	Asp	47
Q	Gln	31
E	Glu	51

Using the amino acid composition shown in Table 6, a human codon-optimized coding region which encodes SEQ ID NO:4 can be designed by any of the methods discussed herein. In the first approach, each amino acid is assigned the most frequent codon used in the human genome for that amino acid. According to this method, codons are assigned to the coding region encoding SEQ ID NO:4 as follows: the 24 phenylalanine codons are TTC, the 62 leucine codons are CTG, the 57 isoleucine codons are ATC, the 10 methionine codons are ATG, the 43 valine codons are GTG, the 72 serine codons are AGC, the 29 proline codons are CCC, the 58 threonine codons are ACC, the 41 alanine codons are GCC, the 28 tyrosine codons are TAC, the 10 histidine codons are CAC, the 31 glutamine codons are CAG, the 69 asparagine codons are AAC, the 60 lysine codons are AAG, the 47 aspartic acid codons are GAC, the 51 glutamic acid codons are GAG, the 7 tryptophan codons are TGG, the 29 arginine codons are CGG, AGA, or AGG (the frequencies of usage of these three codons in the human genome are not significantly different), and the 36 glycine codons are GGC. The codon-optimized PA coding region designed by this method is presented herein as SEQ ID NO:21.

Alternatively, a human codon-optimized coding region which encodes SEQ ID NO:4 can be designed by randomly assigning each of any given amino acid a codon based on the frequency that codon is used in the human genome. These frequencies are shown in Table 2 above. Using this latter method, codons are assigned to the coding region encoding SEQ ID NO:4 as follows: about 11 of the 24 phenylalanine codons are TTT, and about 13 of the phenylalanine codons are TTC; about 5 of the 62 leucine codons are TTA, about 8 of the leucine codons are TTG, about 8 of the leucine codons are CTT, about 12 of the leucine codons are CTC, about 4 of the leucine codons are CTA, and about 25 of the leucine codons are CTG; about 20 of the 57

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isoleucine codons are ATT, about 28 of the isoleucine codons are ATC, and about 9 of the isoleucine codons are ATA; the 10 methionine codons are ATG; about 8 of the 43 valine codons are GTT, about 10 of the valine codons are GTG, about 5 of the valine codons are GTA, and about 20 of the valine
5 codons are GTG; about 13 of the 72 serine codons are TCT, about 16 of the serine codons are TCC, about 11 of the serine codons are TCA, about 4 of the serine codons are TCG, about 11 of the serine codons are AGT, and about 17 of the serine codons are AGC; about 8 of the 29 proline codons are CCT, about 10 of the proline codons are CCC, about 8 of the proline codons are
10 CCA, and about 3 of the proline codons are CCG; about 14 of the 58 threonine codons are ACT, about 21 of the threonine codons are ACC, about 16 of the threonine codons are ACA, and about 7 of the threonine codons are ACG; about 11 of the 41 alanine codons are GGT, about 17 of the alanine codons are GCC, about 9 of the alanine codons are GCA, and about 4 of the alanine
15 codons are GCG; about 12 of the 28 tyrosine codons are TAT and about 16 of the tyrosine codons are TAC; about 4 of the 10 histidine codons are CAT and about 6 of the histidine codons are CAC; about 8 of the 31 glutamine codons are CAA and about 23 of the glutamine codons are CAG; about 32 of the 69 asparagine codons are AAT and about 37 of the asparagine codons are AAC;
20 about 25 of the 60 lysine codons are AAA and about 35 of the lysine codons are AAG; about 22 of the 47 aspartic acid codons are GAT and about 25 of the aspartic acid codons are GAC; about 21 of the 51 glutamic acid codons are GAA and about 30 of the glutamic acid codons are GAG; the 7 tryptophan codons are TGG; about 2 of the 29 arginine codons are CGT, about 6 of the arginine codons are CGC, about 3 of the arginine codons are CGA, about 6 of the arginine codons are CGG, about 6 of the arginine codons are AGA, and
25 about 6 of the arginine codons are AGG; and about 6 of the 36 glycine codons are GGT, about 12 of the glycine codons are GGC, about 9 of the glycine codons are GGA, and about 9 of the glycine codons are GGG.

30 As described above, the term "about" means that the number of amino acids encoded by a certain codon may be one more or one less than the

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number given. It would be understood by those of ordinary skill in the art that the total number of any amino acid in the polypeptide sequence must remain constant, therefore, if there is one "more" of one codon encoding a give amino acid, there would have to be one "less" of another codon encoding that same amino acid.

Representative codon-optimized coding regions encoding SEQ ID NO:4, optimized according to codon usage in humans designed by this method are presented herein as SEQ ID NO:23, SEQ ID NO:24, and SEQ ID NO:25.

In certain embodiments, the present invention provides an isolated polynucleotide comprising a nucleic acid fragment which encodes at least 10, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 95, or at least 100 or more contiguous amino acids of SEQ ID NO:4, where the nucleic acid fragment is a fragment of a codon-optimized coding region encoding SEQ ID NO:4. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human.

Further provided is an isolated polynucleotide comprising a nucleic acid fragment of a codon-optimized coding region encoding SEQ ID NO:4, where the nucleic acid fragment encodes amino acids 199 to 764 of SEQ ID NO:4. This polypeptide fragment is the 63-kD furin cleavage product (PA63) of the 82-kD protective antigen precursor polypeptide (PA83). The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human. Included in this embodiment are nucleic acid fragments of a human codon-optimized coding region encoding SEQ ID NO:4, selected from: nucleotides 82 to 1779 of SEQ ID NO:1 (shown in Fig. 1), nucleotides 595 to 2292 of SEQ ID NO:23, nucleotides 595 to 2292 of SEQ ID NO:24, and nucleotides 595 to 2292 of SEQ ID NO:25.

Further provided is an isolated polynucleotide comprising a nucleic acid fragment of a codon-optimized coding region encoding SEQ ID NO:4,

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where the nucleic acid fragment encodes amino acids 30 to 764 of SEQ ID NO:4. This polypeptide fragment is the mature full-length PA, *i.e.*, PA83. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human. Included in this embodiment are nucleic acid fragments of a human codon-optimized coding region encoding SEQ ID NO:4, selected from: nucleotides 88 to 2292 of SEQ ID NO:23; nucleotides 88 to 2292 of SEQ ID NO:24, and nucleotides 88 to 2292 of SEQ ID NO:25.

In certain embodiments, the present invention provides an isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to PA63, *i.e.*, amino acids 199 to 764 of SEQ ID NO:4, and where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID NO:4. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human.

Further provided is an isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide variant of PA63, *i.e.*, amino acids 199 to 764 of SEQ ID NO:4, in which the amino acids corresponding to amino acids 342 and 343 of SEQ ID NO:4 have been deleted, and where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID NO:4. This variation in the amino acid sequence of PA63 eliminates two phenylalanine residues thought to be important in forming the pore in the *B. anthracis* lethal toxin. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human. Included in this embodiment is a nucleic acid fragment which is a variant of a human codon-optimized coding region encoding SEQ ID NO:4, where the nucleic acid fragment encodes amino acids 24 to 564 of SEQ ID NO:6 (shown in Fig. 2). Also included in this embodiment is a nucleic acid fragment comprising, or

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alternatively consisting of nucleotides 82 to 1773 of SEQ ID NO:5 (shown in Fig. 2).

Further provided is an isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide variant of PA63, *i.e.*, amino acids 199 to 764 of SEQ ID NO:4, in which the asparagine residues at positions corresponding to amino acids 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 have been each replaced with an amino acids other than asparagine, and where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID NO:4. In certain embodiments, the asparagine residues at positions corresponding to amino acids 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 have been each replaced with glutamine residues, where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID NO:4. Either of these variations in the amino acid sequence of PA63 removes adventitious substrates for asparagine-linked glycosylation present in the amino acid sequence. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human. Included in this embodiment is a nucleic acid fragment which is a variant of a human codon-optimized coding region encoding SEQ ID NO:4, where the nucleic acid fragment encodes amino acids 24 to 566 of SEQ ID NO:18 (shown in Fig. 7). Also included in this embodiment is a nucleic acid fragment comprising, or alternatively consisting of nucleotides 82 to 1779 of SEQ ID NO:17 (shown in Fig. 7).

Further provided is an isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide variant of PA63, *i.e.*, amino acids 199 to 764 of SEQ ID NO:4, in which the amino acids corresponding to amino acids 342 and 343 of SEQ ID NO:4 have been deleted, where the asparagine residues at positions corresponding to amino acids 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 have been each replaced with an amino acids other than asparagine, for example, glutamine, and where the nucleic acid fragment is a variant of a codon-optimized coding region

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encoding SEQ ID NO:4. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human.

5 In certain embodiments, the present invention provides an isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to PA83, *i.e.*, amino acids 30 to 764 of SEQ ID NO:4, and where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID
10 NO:4. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human.

Further provided is an isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide variant of PA83, *i.e.*, amino acids
15 30 to 764 of SEQ ID NO:4, in which the amino acids corresponding to amino acids 192 to 197 of SEQ ID NO:4 have been deleted, and where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID NO:4. This variation in the amino acid sequence of PA83 eliminates the furin cleavage site in PA83, and thus the encoded polypeptide cannot be
20 cleaved as a substrate for furin, and cannot form the pore of the lethal toxin of *B. anthracis*. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human. Included in this embodiment is a nucleic acid fragment which is a variant of a human codon-optimized coding
25 region encoding SEQ ID NO:4, where the nucleic acid fragment encodes amino acids 24 to 752 of SEQ ID NO:8 (shown in Fig. 3). Also included in this embodiment is a nucleic acid fragment comprising, or alternatively consisting of nucleotides 82 to 2268 of SEQ ID NO:7 (shown in Fig. 3).

Further provided is an isolated polynucleotide comprising a nucleic
30 acid fragment which encodes a polypeptide variant of PA83, *i.e.*, amino acids 30 to 764 of SEQ ID NO:4, in which the asparagine residues at positions

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corresponding to amino acids 39, 153, 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 have been each replaced with an amino acids other than asparagine, and where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID NO:4. In certain
5 embodiments, the asparagine residues at positions corresponding to amino acids 39, 153, 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 have been each replaced with glutamine residues, where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID NO:4. Either of these variations in the amino acid sequence of PA83 removes
10 adventitious substrates for asparagine-linked glycosylation present in the amino acid sequence. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human.

Further provided is an isolated polynucleotide comprising a nucleic
15 acid fragment which encodes a polypeptide variant of PA83, *i.e.*, amino acids 30 to 764 of SEQ ID NO:4, in which the amino acids corresponding to amino acids 192 to 197 of SEQ ID NO:4 have been deleted, where the asparagine residues at positions corresponding to amino acids 39, 153, 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 have been each
20 replaced with an amino acids other than asparagine, for example, glutamine, and where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID NO:4. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human.

25 The present invention provides isolated polynucleotides comprising codon-optimized coding regions of *Bacillus anthracis* LF, or fragments, variants, or derivatives thereof. In certain embodiments described herein, a codon-optimized coding region encoding SEQ ID NO:12 is optimized according to codon usage in humans (*Homo sapiens*). Alternatively, a codon-
30 optimized coding region encoding SEQ ID NO:12 may be optimized according to codon usage in any plant, animal, or microbial species.

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Codon-optimized coding regions encoding SEQ ID NO:12, optimized according to codon usage in humans are designed as follows. The amino acid composition of SEQ ID NO:12 is shown in Table 7.

TABLE 7

Amino Acid		Number in SEQ ID NO:12
A	Ala	34
R	Arg	27
C	Cys	1
G	Gly	35
H	His	21
I	Ile	74
L	Leu	80
K	Lys	86
M	Met	10
F	Phe	29
P	Pro	21
S	Ser	54
T	Thr	28
W	Trp	5
Y	Tyr	35
V	Val	40
N	Asn	54
D	Asp	55
Q	Gln	41
E	Glu	79

5

Using the amino acid composition shown in Table 7, a human codon-optimized coding region which encodes SEQ ID NO:12 can be designed by any of the methods discussed herein. In the first approach, each amino acid is assigned the most frequent codon used in the human genome for that amino acid. According to this method, codons are assigned to the coding region encoding SEQ ID NO:4 as follows: the 29 phenylalanine codons are TTC, the 80 leucine codons are CTG, the 74 isoleucine codons are ATC, the 10 methionine codons are ATG, the 43 valine codons are GTG, the 54 serine codons are AGC, the 21 proline codons are CCC, the 28 threonine codons are

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ACC, the 34 alanine codons are GCC, the 35 tyrosine codons are TAC, the 21 histidine codons are CAC, the 41 glutamine codons are CAG, the 54 asparagine codons are AAC, the 86 lysine codons are AAG, the 55 aspartic acid codons are GAC, the 79 glutamic acid codons are GAG, the 5 tryptophan codons are TGG, the 27 arginine codons are CGG, AGA, or AGG (the frequencies of usage of these three codons in the human genome are not significantly different), and the 35 glycine codons are GGC. The codon-optimized LF coding region designed by this method is presented herein as SEQ ID NO:22.

Alternatively, a human codon-optimized coding region which encodes SEQ ID NO:12 can be designed by randomly assigning each of any given amino acid a codon based on the frequency that codon is used in the human genome. These frequencies are shown in Table 2 above. Using this latter method, codons are assigned to the coding region encoding SEQ ID NO:12 as follows: about 13 of the 29 phenylalanine codons are TTT and about 16 of the phenylalanine codons are TTC; about 6 of the 80 leucine codons are TTA, about 10 of the leucine codons are TTG, about 10 of the leucine codons are CTT, about 16 of the leucine codons are CTC, about 6 of the leucine codons are CTA, and about 32 of the leucine codons are CTG; about 26 of the 74 isoleucine codons are ATT, about 36 of the isoleucine codons are ATC, and about 12 of the isoleucine codons are ATA; the 10 methionine codons are ATG; about 7 of the 40 valine codons are GTT, about 9 of the valine codons are GTG, about 5 of the valine codons are GTA, and about 19 of the valine codons are GTG; about 10 of the 54 serine codons are TCT, about 12 of the serine codons are TCC, about 8 of the serine codons are TCA, about 3 of the serine codons are TCG, about 8 of the serine codons are AGT, and about 13 of the serine codons are AGC; about 6 of the 21 proline codons are CCT, about 7 of the proline codons are CCC, about 6 of the proline codons are CCA, and about 2 of the proline codons are CCG; about 7 of the 28 threonine codons are ACT, about 10 of the threonine codons are ACC, about 8 of the threonine codons are ACA, and about 3 of the threonine codons are ACG; about 9 of the

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34 alanine codons are GGT, about 14 of the alanine codons are GCC, about 8 of the alanine codons are GCA, and about 3 of the alanine codons are GCG; about 15 of the 35 tyrosine codons are TAT and about 20 of the tyrosine codons are TAC; about 9 of the 21 histidine codons are CAT and about 12 of the histidine codons are CAC; about 10 of the 41 glutamine codons are CAA and about 31 of the glutamine codons are CAG; about 25 of the 54 asparagine codons are AAT and about 29 of the asparagine codons are AAC; about 36 of the 86 lysine codons are AAA and about 50 of the lysine codons are AAG; about 25 of the 55 aspartic acid codons are GAT and about 30 of the aspartic acid codons are GAC; about 33 of the 79 glutamic acid codons are GAA and about 46 of the glutamic acid codons are GAG; the single cysteine codon is either TGT or TGC; the 5 tryptophan codons are TGG; about 2 of the 27 arginine codons are CGT, about 5 of the arginine codons are CGC, about 3 of the arginine codons are CGA, about 6 of the arginine codons are CGG, about 6 of the arginine codons are AGA, and about 5 of the arginine codons are AGG; and about 6 of the 35 glycine codons are GGT, about 12 of the glycine codons are GGC, about 8 of the glycine codons are GGA, and about 9 of the glycine codons are GGG.

As described above, the term "about" means that the number of amino acids encoded by a certain codon may be one more or one less than the number given. It would be understood by those of ordinary skill in the art that the total number of any amino acid in the polypeptide sequence must remain constant, therefore, if there is one "more" of one codon encoding a give amino acid, there would have to be one "less" of another codon encoding that same amino acid.

Representative codon-optimized coding regions encoding SEQ ID NO:12, optimized according to codon usage in humans designed by this method are presented herein as SEQ ID NO:26, SEQ ID NO:27, and SEQ ID NO:28.

In certain embodiments, the present invention provides an isolated polynucleotide comprising a nucleic acid fragment which encodes at least 10,

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at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 95, or at least 100 or more contiguous amino acids of SEQ ID NO:12, where the nucleic acid fragment is a fragment of a codon-optimized coding region encoding SEQ ID NO:12. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human.

Further provided is an isolated polynucleotide comprising a nucleic acid fragment of a codon-optimized coding region encoding SEQ ID NO:12, where the nucleic acid fragment encodes amino acids 34 to 809 of SEQ ID NO:12. This polypeptide fragment is the mature form of *B. anthracis* LF. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human. Included in this embodiment are nucleic acid fragments of a human codon-optimized coding region encoding amino acids 34 to 809 of SEQ ID NO:12, selected from: nucleotides 100 to 2427 of SEQ ID NO:26, nucleotides 100 to 2427 of SEQ ID NO:27, and nucleotides 100 to 2427 of SEQ ID NO:28.

Further provided is an isolated polynucleotide comprising a nucleic acid fragment of a codon-optimized coding region encoding SEQ ID NO:12, where the nucleic acid fragment encodes amino acids 34 to 583 of SEQ ID NO:12. This polypeptide fragment encodes domains I-III of mature *B. anthracis* LF, but not domain IV, the protease domain. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human. Included in this embodiment are nucleic acid fragments of a human codon-optimized coding region encoding SEQ ID NO:12, selected from: nucleotides 82 to 1731 of SEQ ID NO:13 (shown in Fig. 5), nucleotides 100 to 1752 of SEQ ID NO:26, nucleotides 100 to 1752 of SEQ ID NO:27, and nucleotides 100 to 1752 of SEQ ID NO:28.

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Further provided is an isolated polynucleotide comprising a nucleic acid fragment of a codon-optimized coding region encoding SEQ ID NO:12, where the nucleic acid fragment encodes amino acids 34 to 254 of SEQ ID NO:12. This polypeptide fragment encodes a portion of domain I of mature *B. anthracis* LF, that directly binds to PA63. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human. Included in this embodiment are nucleic acid fragments of a human codon-optimized coding region encoding SEQ ID NO:12, selected from: nucleotides 82 to 744 of SEQ ID NO:15 (shown in Fig. 6), nucleotides 100 to 762 of SEQ ID NO:26, nucleotides 100 to 762 of SEQ ID NO:27, and nucleotides 100 to 762 of SEQ ID NO:28.

In certain embodiments, the present invention provides an isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to LF, i.e., amino acids 34 to 809 of SEQ ID NO:12, and where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID NO:12. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human.

Further provided is an isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide variant of LF, i.e., amino acids 34 to 809 of SEQ ID NO:12, in which the histidine residues corresponding to amino acids 719 and 723 of SEQ ID NO:12 have been deleted, and replaced with an amino acid other than histidine, and/or the glutamic acid residue corresponding to amino acid 720 of SEQ ID NO:12 has been deleted and replaced with an amino acid other than glutamic acid, where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID NO:12. In certain embodiments, the histidine residues corresponding to amino acids 719 and 723 of SEQ ID NO:12 have been deleted, and replaced with

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alanine residues, and/or the glutamic acid residue corresponding to amino acid 720 of SEQ ID NO:12 has been deleted and replaced with an aspartic acid residue, where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID NO:12. Any of these variations in the amino acid sequence of LF, either alone or in combination, eliminate the protease activity of LF. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human. Included in this embodiment is a nucleic acid fragment which is a variant of a human codon-optimized coding region encoding SEQ ID NO:12, where the nucleic acid fragment encodes amino acids 24 to 799 of SEQ ID NO:10 (shown in Fig. 4). Also included in this embodiment is a nucleic acid fragment comprising, or alternatively consisting of nucleotides 82 to 2409 of SEQ ID NO:9 (shown in Fig. 4).

Further provided is an isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide variant of LF, *i.e.*, amino acids 34 to 809 of SEQ ID NO:12, in which the asparagine residues at positions corresponding to amino acids 62, 212, 286, 478, 712, 736, and 757 of SEQ ID NO:12 have been each replaced with an amino acids other than asparagine, and where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID NO:12. In certain embodiments, the asparagine residues at positions corresponding to amino acids 62, 212, 286, 478, 712, 736, and 757 of SEQ ID NO:12 have been each replaced with glutamine residues, where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID NO:12. Either of these variations in the amino acid sequence of LF remove adventitious substrates for asparagine-linked glycosylation present in the amino acid sequence. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian species, for example human.

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Further provided is an isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide variant of LF, *i.e.*, amino acids 34 to 809 of SEQ ID NO:12, in which the histidine residues corresponding to amino acids 719 and 723 of SEQ ID NO:12 have been deleted, and replaced
5 with an amino acid other than histidine, and/or the glutamic acid residue corresponding to amino acid 720 of SEQ ID NO:12 has been deleted and replaced with an amino acid other than glutamic acid, and the asparagine residues at positions corresponding to amino acids 62, 212, 286, 478, 712, 736, and 757 of SEQ ID NO:12 have been each replaced with an amino acids
10 other than asparagine, and where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID NO:12. In certain embodiments, the histidine residues corresponding to amino acids 719 and 723 of SEQ ID NO:12 have been deleted, and replaced with alanine residues, and/or the glutamic acid residue corresponding to amino acid 720 of SEQ ID
15 NO:12 has been deleted and replaced with an aspartic acid residue, and the asparagine residues at positions corresponding to amino acids 62, 212, 286, 478, 712, 736, and 757 of SEQ ID NO:12 have been each replaced with glutamine residues, where the nucleic acid fragment is a variant of a codon-optimized coding region encoding SEQ ID NO:12. Any of these variations in
20 the amino acid sequence of LF, either alone or in combination, eliminate the protease activity of LF, and also, adventitious substrates for asparagine-linked glycosylation present in the amino acid sequence have been removed. The codon optimized coding region can be optimized according to codon usage in any species, for example any vertebrate species, for example any mammalian
25 species, for example human. Included in this embodiment is a nucleic acid fragment which is a variant of a human codon-optimized coding region encoding SEQ ID NO:12, where the nucleic acid fragment encodes amino acids 24 to 799 of SEQ ID NO:20 (shown in Fig. 8). Also included in this embodiment is a nucleic acid fragment comprising, or alternatively consisting
30 of nucleotides 82 to 2409 of SEQ ID NO:19 (shown in Fig. 8).

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In this manner, the present invention provides a method of enhancing the level of polypeptide expression from delivered polynucleotides *in vivo* and/or facilitating uptake of the polynucleotides by the cells of a desired species, for example a vertebrate species, for example a mammalian species, for example humans. Accordingly, the present invention provides a method of treatment and prevention against *Bacillus anthracis* infection.

Methods and Administration

The present invention further provides methods for delivering a polypeptide into a vertebrate, which comprise administering to a vertebrate one or more of the compositions described herein; such that upon administration of compositions such as those described herein, a *B. anthracis* polypeptide is expressed in the vertebrate, in an amount sufficient generate an immune response to *B. anthracis*.

The term "vertebrate" is intended to encompass a singular "vertebrate" as well as plural "vertebrates," and comprises mammals and birds, as well as fish, reptiles, and amphibians.

The term "mammal" is intended to encompass a singular "mammal" and plural "mammals," and includes, but is not limited to humans; primates such as apes, monkeys, orangutans, and chimpanzees; canids such as dogs and wolves; felids such as cats, lions, and tigers; equids such as horses, donkeys, and zebras, food animals such as cows, pigs, and sheep; ungulates such as deer and giraffes; and ursids such as bears. In particular, the mammal can be a human subject, a food animal or a companion animal.

The present invention further provides a method for generating, enhancing or modulating an immune response to *B. anthracis* comprising administering to a vertebrate one or more of the compositions described herein. In this method, the composition includes an isolated polynucleotide comprising a human codon-optimized coding region encoding a polypeptide of *Bacillus anthracis*, or a nucleic acid fragment of such a coding region

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encoding a fragment, variant, or derivative thereof. The polynucleotides are incorporated into the cells of the vertebrate *in vivo*, and an antigenic amount of the *Bacillus anthracis* polypeptide, or fragment, variant, or derivative thereof, is produced *in vivo*. Upon administration of the composition according to this method, the *Bacillus anthracis* polypeptide is expressed in the vertebrate in an amount sufficient to elicit an immune response. Such an immune response might be used, for example, to generate antibodies to *B. anthracis* for use in diagnostic assays or as laboratory reagents.

The present invention further provides a method for generating, enhancing, or modulating a protective and/or therapeutic immune response to *B. anthracis* in a vertebrate, comprising administering to a vertebrate in need of therapeutic and/or preventative immunity one or more of the compositions described herein. In this method, the composition includes an isolated polynucleotide comprising a human codon-optimized coding region encoding a polypeptide of *Bacillus anthracis*, or a nucleic acid fragment of such a coding region encoding a fragment, variant, or derivative thereof. The polynucleotides are incorporated into the cells of the vertebrate *in vivo*, and an immunologically effective amount of the *Bacillus anthracis* polypeptide, or fragment or variant is produced *in vivo*. Upon administration of the composition according to this method, the *Bacillus anthracis* polypeptide is expressed in the vertebrate in a therapeutically or prophylactically effective amount.

As used herein, an "immune response" refers to the ability of a vertebrate to elicit an immune reaction to a composition delivered to that vertebrate. Examples of immune responses include an antibody response or a cellular, *e.g.*, T-cell, response. One or more compositions of the present invention may be used to treat a vertebrate prophylactically, *e.g.*, as a prophylactic vaccine, to establish or enhance immunity to *B. anthracis* in a healthy vertebrate prior to exposure to *B. anthracis* or contraction of anthrax disease, thus preventing the disease or reducing the severity of disease symptoms. One or more compositions of the present invention may also be

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used to treat a vertebrate already exposed to *B. anthracis*, or already suffering from anthrax disease to further stimulate the immune system of the vertebrate, thus reducing or eliminating the symptoms associated with that disease or disorder. As defined herein, "treatment of a vertebrate" refers to the use of
5 One or more compositions of the present invention to prevent, cure, retard, or reduce the severity of anthrax disease symptoms in a vertebrate, and/or result in no worsening of anthrax disease over a specified period of time. It is not required that any composition of the present invention provide total immunity to *B. anthracis* or totally cure or eliminate all anthrax disease symptoms. As
10 used herein, a "a vertebrate in need of therapeutic and/or preventative immunity" refers to a vertebrate which it is desirable to treat, *i.e.*, to prevent, cure, retard, or reduce the severity of anthrax disease symptoms, and/or result in no worsening of anthrax disease over a specified period of time.

In other embodiments, one or more compositions of the present
15 invention are utilized in a "prime boost" regimen. In these embodiments, one or more polynucleotide vaccine compositions of the present invention are delivered to a vertebrate, thereby priming the immune response of the vertebrate to *B. anthracis*, and then a second immunogenic composition is utilized as a boost vaccination. One or more polynucleotide vaccine
20 compositions of the present invention are used to prime immunity, and then a second immunogenic composition, *e.g.*, a recombinant viral vaccine or vaccines, a different polynucleotide vaccine, one or more purified subunit *Bacillus anthracis* proteins, *e.g.*, PA or LF or a variant, fragment, or derivative thereof, or the existing AVA anthrax vaccine, is used to boost the
25 anti-*Bacillus anthracis* immune response. The polynucleotide vaccine compositions may comprise one or more vectors for expression of one or more *Bacillus anthracis* lethal toxin genes as described herein. In addition, polynucleotide prime vaccine and the later boost vaccine elicit an immune response to the same or similar antigens, or they may be to different antigens.

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In another embodiment, vectors are prepared for expression in the recombinant virus vaccine and in transfected mammalian cells as part of a polynucleotide vaccine.

5 The terms "priming" or "primary" and "boost" or "boosting" are used herein to refer to the initial and subsequent immunizations, respectively, *i.e.*, in accordance with the definitions these terms normally have in immunology.

 Sterile immunity is defined herein as the ability to completely inhibit the germination of anthrax spores into bacteria. If germination occurs, the bacteria produce Letx and surviving rabbits immunized against the PA antigen
10 would be expected to generate a response to LF. Likewise, rabbits immunized with LF should have a measurable response to PA.

 Antibodies induced by recombinant PA or by the commercial anthrax vaccine, AVA, have been shown to have potential activities other than neutralization, that may affect the outcome of an infection by anthrax. Among
15 these potential activities is the effect of preventing germination of bacteria from the spores. (Welkos, S. *et al. Microbiology*. 147: 1677-85 (2001)). DNA vaccination may induce levels of antibody consistent with those that prevent germination. The absence of an increase in LF, PA, or neutralization titers, following infection, has been observed in animals vaccinated with DNA
20 vaccines. This is in contrast to animals vaccinated twice with a commercial anthrax vaccine, AVA. While not being bound by theory, the DNA vaccine may induce antibodies that possess novel protective activities independent of lethal toxin neutralization.

 In certain embodiments, one or more compositions of the present
25 invention are delivered to a vertebrate by methods described herein, thereby achieving an effective immune response, and or an effective therapeutic or preventative immune response.

 More specifically, the compositions of the present invention may be administered to any tissue of a vertebrate, including, but not limited to,
30 muscle, skin, brain tissue, lung tissue, liver tissue, spleen tissue, bone marrow tissue, thymus tissue, heart tissue, *e.g.*, myocardium, endocardium, and

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pericardium, lymph tissue, blood tissue, bone tissue, pancreas tissue, kidney tissue, gall bladder tissue, stomach tissue, intestinal tissue, testicular tissue, ovarian tissue, uterine tissue, vaginal tissue, rectal tissue, nervous system tissue, eye tissue, glandular tissue, tongue tissue, and connective tissue, e.g., cartilage.

Furthermore, the compositions of the present invention may be administered to any internal cavity of a vertebrate, including, but not limited to, the lungs, the mouth, the nasal cavity, the stomach, the peritoneal cavity, the intestine, any heart chamber, veins, arteries, capillaries, lymphatic cavities, the uterine cavity, the vaginal cavity, the rectal cavity, joint cavities, ventricles in brain, spinal canal in spinal cord, the ocular cavities, the lumen of a duct of a salivary gland or a liver. When the compositions of the present invention is administered to the lumen of a duct of a salivary gland or a liver, the desired polypeptide is encoded in each of the salivary gland and the liver such that the polypeptide is delivered into the blood stream of the vertebrate from each of the salivary gland and the liver. Certain modes for administration to secretory organs of a gastrointestinal system using the salivary gland, liver and pancreas to release a desired polypeptide into the bloodstream is disclosed in U.S. Patent Nos. 5,837,693 and 6,004,944, both of which are incorporated herein by reference in their entireties.

In one embodiment, the compositions are administered to muscle, either skeletal muscle or cardiac muscle, or lung tissue. Specific, but non-limiting modes for administration to lung tissue are disclosed in Wheeler, C.J., *et al.*, *Proc. Natl. Acad. Sci. USA* 93:11454-11459 (1996), which is incorporated herein by reference in its entirety.

According to the disclosed methods, compositions of the present invention can be administered by intramuscular (i.m.), subcutaneous (s.c.), or intrapulmonary routes. Other suitable routes of administration include, but not limited to intratracheal, transdermal, intraocular, intranasal, inhalation, intracavity, intravenous (i.v.), intraductal (e.g., into the pancreas) and intraparenchymal (i.e., into any tissue) administration. Transdermal delivery

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includes, but not limited to intradermal (e.g., into the dermis or epidermis), transdermal (e.g., percutaneous) and transmucosal administration (i.e., into or through skin or mucosal tissue). Intracavity administration includes, but not limited to administration into oral, vaginal, rectal, nasal, peritoneal, or intestinal cavities as well as, intrathecal (i.e., into spinal canal), intraventricular (i.e., into the brain ventricles or the heart ventricles), intraatrial (i.e., into the heart atrium) and sub arachnoid (i.e., into the sub arachnoid spaces of the brain) administration.

Any mode of administration can be used so long as the mode results in the expression of the desired peptide or protein, in the desired tissue, in an amount sufficient to generate an immune response to *B. anthracis* and/or to generate a prophylactically or therapeutically effective immune response to *B. anthracis* in a vertebrate in need of such response. Administration means of the present invention include needle injection, catheter infusion, biolistic injectors, particle accelerators (e.g., "gene guns" or pneumatic "needleless" injectors) Med-E-Jet (Vahlsing, H., *et al.*, *J. Immunol. Methods* 171,11-22 (1994)), Pigjet (Schrijver, R., *et al.*, *Vaccine* 15, 1908-1916 (1997)), Biojector (Davis, H., *et al.*, *Vaccine* 12, 1503-1509 (1994); Gramzinski, R., *et al.*, *Mol. Med.* 4, 109-118 (1998)), AdvantaJet (Linmayer, I., *et al.*, *Diabetes Care* 9:294-297 (1986)), Medi-jector (Martins, J., and Roedl, E. *J. Occup. Med.* 21:821-824 (1979)), gelfoam sponge depots, other commercially available depot materials (e.g., hydrogels), osmotic pumps (e.g., Alza minipumps), oral or suppositorial solid (tablet or pill) pharmaceutical formulations, topical skin creams, and decanting, use of polynucleotide coated suture (Qin, Y., *et al.*, *Life Sciences* 65, 2193-2203 (1999)) or topical applications during surgery. Certain modes of administration are intramuscular needle-based injection and pulmonary application via catheter infusion. Each of the references cited in this paragraph is incorporated herein by reference in its entirety.

Determining an effective amount of one or more compositions of the present invention depends upon a number of factors including, for example, the antigen being expressed, e.g., PA or LF or fragments, variants, or

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derivatives thereof, the age and weight of the subject, the precise condition requiring treatment and its severity, and the route of administration. Based on the above factors, determining the precise amount, number of doses, and timing of doses are within the ordinary skill in the art and will be readily
5 determined by the attending physician or veterinarian.

Compositions of the present invention may include various salts, excipients, delivery vehicles and/or auxiliary agents as are disclosed, *e.g.*, in U.S. Patent Application Publication 2002/0019358, published February 14, 2002, which is incorporated herein by reference in its entirety.

10 Furthermore, compositions of the present invention may include one or more transfection facilitating compounds that facilitate delivery of polynucleotides to the interior of a cell, and/or to a desired location within a cell. As used herein, the terms "transfection facilitating compound," "transfection facilitating agent," and "transfection facilitating material" are
15 synonymous, and may be used interchangeably. It should be noted that certain transfection facilitating compounds may also be "adjuvants" as described *infra*, *i.e.*, in addition to facilitating delivery of polynucleotides to the interior of a cell, the compound acts to alter or increase the immune response to the antigen encoded by that polynucleotide. Examples of the transfection
20 facilitating compounds include, but are not limited to inorganic materials such as calcium phosphate, alum (aluminum sulfate), and gold particles (*e.g.*, "powder" type delivery vehicles); peptides that are, for example, cationic, intercell targeting (for selective delivery to certain cell types), intracell targeting (for nuclear localization or endosomal escape), and amphoteric (helix forming or pore forming); proteins that are, for example, basic (*e.g.*, positively charged) such as histones, targeting (*e.g.*, asialoglycoprotein), viral (*e.g.*, Sendai virus coat protein), and pore-forming; lipids that are, for example, cationic (*e.g.*, DMRPE, DOSPA, DC-Chol), basic (*e.g.*, steryl amine), neutral (*e.g.*, cholesterol), anionic (*e.g.*, phosphatidyl serine), and zwitterionic (*e.g.*, DOPE, DOPC); and polymers such as dendrimers, star-polymers, "homogenous"
25 poly-amino acids (*e.g.*, poly-lysine, poly-arginine), "heterogenous"

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poly-amino acids (e.g., mixtures of lysine & glycine), co-polymers, polyvinylpyrrolidinone (PVP), and polyethylene glycol (PEG). A transfection facilitating material can be used alone or in combination with one or more other transfection facilitating materials. Two or more transfection facilitating materials can be combined by chemical bonding (e.g., covalent and ionic such as in lipidated polylysine, PEGylated polylysine) (Toncheva, *et al.*, *Biochim. Biophys. Acta* 1380(3):354-368 (1988)), mechanical mixing (e.g., free moving materials in liquid or solid phase such as "polylysine + cationic lipids") (Gao and Huang, *Biochemistry* 35:1027-1036 (1996); Trubetskoy, *et al.*, *Biochem. Biophys. Acta* 1131:311-313 (1992)), and aggregation (e.g., co-precipitation, gel forming such as in cationic lipids + poly-lactide co-galactide, and polylysine + gelatin).

One category of transfection facilitating materials is cationic lipids. Examples of cationic lipids are 5-carboxyspermylglycine dioctadecylamide (DOGS) and dipalmitoyl-phosphatidylethanolamine-5-carboxyspermylamide (DPPES). Cationic cholesterol derivatives are also useful, including {3 β -[N-N',N'-dimethylamino)ethane]-carbomoyl}-cholesterol (DC-Chol). Dimethyldioctadecyl-ammonium bromide (DDAB), N-(3-aminopropyl)-N,N-(bis-(2-tetradecyloxyethyl))-N-methyl-ammonium bromide (PA-DEMO), N-(3-aminopropyl)-N,N-(bis-(2-dodecyloxyethyl))-N-methyl-ammonium bromide (PA-DELO), N,N,N-tris-(2-dodecyloxy)ethyl-N-(3-amino)propyl-ammonium bromide (PA-TELO), and N¹-(3-aminopropyl)((2-dodecyloxy)ethyl)-N²-(2-dodecyloxy)ethyl-1-piperazinaminium bromide (GA-LOE-BP) can also be employed in the present invention.

Non-diether cationic lipids, such as DL-1,2-dioleoyl-3-dimethylaminopropyl- β -hydroxyethylammonium (DORI diester), 1-O-oleyl-2-oleoyl-3-dimethylaminopropyl- β -hydroxyethylammonium (DORI ester/ether), and their salts promote *in vivo* gene delivery. In some embodiments, cationic lipids comprise groups attached via a heteroatom attached to the quaternary ammonium moiety in the head group. A glycyl spacer can connect the linker to the hydroxyl group.

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Specific, but non-limiting cationic lipids for use in certain embodiments of the present invention include DMRIE ((\pm)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide), GAP-DMORIE ((\pm)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide), and GAP-DLRIE ((\pm)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(dodecyloxy)-1-propanaminium bromide).

Other cationic lipids include (\pm)-N,N-dimethyl-N-[2-(sperminecarboxamido)ethyl]-2,3-bis(dioleyloxy)-1-propaniminium pentahydrochloride (DOSPA), (\pm)-N-(2-aminoethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propaniminium bromide (β -aminoethyl-DMRIE or β AE-DMRIE) (Wheeler, *et al.*, *Biochim. Biophys. Acta* 1280:1-11 (1996)), and (\pm)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(dodecyloxy)-1-propaniminium bromide (GAP-DLRIE) (Wheeler, *et al.*, *Proc. Natl. Acad. Sci. USA* 93:11454-11459 (1996)), which have been developed from DMRIE.

Other examples of DMRIE-derived cationic lipids that are useful for the present invention are (\pm)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(decyloxy)-1-propanaminium bromide (GAP-DDRIE), (\pm)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide (GAP-DMRIE), (\pm)-N-((N"-methyl)-N"-ureyl)propyl-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide (GMU-DMRIE), (\pm)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(dodecyloxy)-1-propanaminium bromide (DLRIE), and (\pm)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis-([Z]-9-octadeceneyloxy)propyl-1-propaniminium bromide (HP-DORIE).

In the embodiments where the immunogenic composition comprises a cationic lipid, the cationic lipid may be mixed with one or more co-lipids. For purposes of definition, the term "co-lipid" refers to any hydrophobic material which may be combined with the cationic lipid component and includes amphipathic lipids, such as phospholipids, and neutral lipids, such as cholesterol. Cationic lipids and co-lipids may be mixed or combined in a number of ways to produce a variety of non-covalently bonded macroscopic

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structures, including, for example, liposomes, multilamellar vesicles, unilamellar vesicles, micelles, and simple films. One non-limiting class of co-lipids are the zwitterionic phospholipids, which include the phosphatidylethanolamines and the phosphatidylcholines. Examples of phosphatidylethanolamines, include DOPE, DMPE and DPyPE. In certain embodiments, the co-lipid is DPyPE, which comprises two phytanoyl substituents incorporated into the diacylphosphatidylethanolamine skeleton.

When a composition of the present invention comprises a cationic lipid and co-lipid, the cationic lipid:co-lipid molar ratio may be from about 9:1 to about 1:9, from about 4:1 to about 1:4, from about 2:1 to about 1:2, or about 1:1.

In order to maximize homogeneity, the cationic lipid and co-lipid components may be dissolved in a solvent such as chloroform, followed by evaporation of the cationic lipid/co-lipid solution under vacuum to dryness as a film on the inner surface of a glass vessel (e.g., a Rotovap round-bottomed flask). Upon suspension in an aqueous solvent, the amphipathic lipid component molecules self-assemble into homogenous lipid vesicles. These lipid vesicles may subsequently be processed to have a selected mean diameter of uniform size prior to complexing with, for example, a codon-optimized polynucleotide of the present invention, according to methods known to those skilled in the art. For example, the sonication of a lipid solution is described in Felgner *et al.*, *Proc. Natl. Acad. Sci. USA* 84,7413-7417 (1987) and in U.S. Pat. No. 5,264,618, the disclosures of which are incorporated herein by reference.

In those embodiments where the composition includes a cationic lipid, polynucleotides of the present invention are complexed with lipids by mixing, for example, a plasmid in aqueous solution and a solution of cationic lipid:co-lipid as prepared herein are mixed. The concentration of each of the constituent solutions can be adjusted prior to mixing such that the desired final plasmid/cationic lipid:co-lipid ratio and the desired plasmid final concentration will be obtained upon mixing the two solutions. The cationic

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lipid:co-lipid mixtures are suitably prepared by hydrating a thin film of the mixed lipid materials in an appropriate volume of aqueous solvent by vortex mixing at ambient temperatures for about 1 minute. The thin films are prepared by admixing chloroform solutions of the individual components to afford a desired molar solute ratio followed by aliquoting the desired volume of the solutions into a suitable container. The solvent is removed by evaporation, first with a stream of dry, inert gas (e.g. argon) followed by high vacuum treatment.

Other hydrophobic and amphiphilic additives, such as, for example, sterols, fatty acids, gangliosides, glycolipids, lipopeptides, liposaccharides, neobees, niosomes, prostaglandins and sphingolipids, may also be included in compositions of the present invention. In such compositions, these additives may be included in an amount between about 0.1 mol % and about 99.9 mol % (relative to total lipid), about 1-50 mol %, or about 2-25 mol %.

Additional embodiments of the present invention are drawn to compositions comprising an auxiliary agent. The present invention is further drawn to methods to use such compositions, methods to make such compositions, and pharmaceutical kits. As used herein, an "auxiliary agent" is a substance included in a composition for its ability to enhance, relative to a composition which is identical *except* for the inclusion of the auxiliary agent, the entry of polynucleotides into vertebrate cells *in vivo*, and/or the *in vivo* expression of polypeptides encoded by such polynucleotides. Auxiliary agents of the present invention include nonionic, anionic, cationic, or zwitterionic surfactants or detergents, in particular, nonionic surfactants or detergents, chelators, DNase inhibitors, agents that aggregate or condense nucleic acids, emulsifying or solubilizing agents, wetting agents, gel-forming agents, and buffers.

Auxiliary agents for use in compositions of the present invention include, but are not limited to non-ionic detergents and surfactants IGEPAL CA 630® CA 630, NONIDET NP-40, Nonidet ® P40, Tween-20®, Tween-80®, Pluronic® F68, Pluronic F77®, Pluronic P65®, Triton X-100™, and

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Triton X-114™; the anionic detergent sodium dodecyl sulfate (SDS); the sugar stachyose; the condensing agent DMSO; and the chelator/DNAse inhibitor EDTA. In certain specific embodiments, the auxiliary agent is DMSO, Nonidet P40, Pluronic F68®, Pluronic F77®, Pluronic P65®, Pluronic L64®,
5 and Pluronic F108®. See, e.g., U.S. Patent Application Publication 20020019358, published February 14, 2002, which is incorporated herein by reference in its entirety.

Compositions of the present invention can be formulated according to known methods. Suitable preparation methods are described, for example, in
10 Remington's Pharmaceutical Sciences, 16th Edition, A. Osol, ed., Mack Publishing Co., Easton, PA (1980), and Remington's Pharmaceutical Sciences, 19th Edition, A.R. Gennaro, ed., Mack Publishing Co., Easton, PA (1995), both of which are incorporated herein by reference in their entireties. Although the composition may be administered as an aqueous solution, it can
15 also be formulated as an emulsion, gel, solution, suspension, lyophilized form, or any other form known in the art. In addition, the composition may contain pharmaceutically acceptable additives including, for example, diluents, binders, stabilizers, and preservatives.

Certain compositions of the present invention may further include one
20 or more known adjuvants. The term "adjuvant" refers to any material having the ability to (1) alter or increase the immune response to a particular antigen or (2) increase or aid an effect of a pharmacological agent. It should be noted, with respect to polynucleotide vaccines, that an "adjuvant," may be a transfection facilitating material. Similarly, certain "transfection facilitating
25 materials" described *supra*, may also be an "adjuvant." An adjuvant may be used with a composition comprising a polynucleotide of the present invention. In a prime-boost regiment, as described herein, an adjuvant may be used with either the priming immunization, the booster immunization, or both. Suitable adjuvants include, but are not limited to, cytokines and growth factors;
30 bacterial components (e.g., endotoxins, in particular superantigens, exotoxins

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and cell wall components); aluminum-based salts; calcium-based salts; silica; polynucleotides; toxoids; serum proteins, viruses and virally-derived materials, poisons, venoms, and cationic lipids.

5 The ability of an adjuvant to increase the immune response to an antigen is typically manifested by a significant increase in immune-mediated protection. For example, an increase in humoral immunity is typically manifested by a significant increase in the titer of antibodies raised to the antigen, and an increase in T-cell activity is typically manifested in increased cell proliferation, or cellular cytotoxicity. An adjuvant may also alter an
10 immune response, for example, by changing a primarily humoral or Th₂ response into a primarily cellular, or Th₁ response.

In certain adjuvant compositions, the adjuvants are cytokines. A composition of the present invention can comprise one or more cytokines, chemokines, or compounds that induce the production of cytokines and
15 chemokines, or a polynucleotide encoding one or more cytokines, chemokines, or compounds that induce the production of cytokines and chemokines. Examples include, but are not limited to granulocyte macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), colony stimulating factor
20 (CSF), erythropoietin (EPO), interleukin 2 (IL-2), interleukin-3 (IL-3), interleukin 4 (IL-4), interleukin 5 (IL-5), interleukin 6 (IL-6), interleukin 7 (IL-7), interleukin 8 (IL-8), interleukin 10 (IL-10), interleukin 12 (IL-12), interleukin 15 (IL-15), interleukin 18 (IL-18), interferon alpha (IFN α), interferon beta (IFN β), interferon gamma (IFN γ), interferon omega (IFN ω),
25 interferon tau (IFN τ), interferon gamma inducing factor I (IGIF), transforming growth factor beta (TGF- β), RANTES (regulated upon activation, normal T-cell expressed and presumably secreted), macrophage inflammatory proteins (e.g., MIP-1 alpha and MIP-1 beta), *Leishmania* elongation initiating factor (LEIF), and Flt-3 ligand.

30 In certain compositions of the present invention, the polynucleotide construct may be complexed with an adjuvant composition comprising (\pm)-N-

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(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE). The composition may also comprise one or more co-lipids, *e.g.*, 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE), 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and/or 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE). An adjuvant composition comprising ;GAP-DMORIE and DPyPE at a 1:1 molar ratio is referred to herein as Vaxfectin™. *See, e.g.*, PCT Publication No. WO 00/57917, which is incorporated herein by reference in its entirety.

Nucleic acid molecules and/or polynucleotides of the present invention, *e.g.*, pDNA, mRNA, linear DNA or oligonucleotides, may be solubilized in any of various buffers. Suitable buffers include, for example, phosphate buffered saline (PBS), normal saline, Tris buffer, and sodium phosphate (*e.g.*, 150 mM sodium phosphate). Insoluble polynucleotides may be solubilized in a weak acid or weak base, and then diluted to the desired volume with a buffer. The pH of the buffer may be adjusted as appropriate. In addition, a pharmaceutically acceptable additive can be used to provide an appropriate osmolarity. Such additives are within the purview of one skilled in the art. For aqueous compositions used *in vivo*, sterile pyrogen-free water can be used. Such formulations will contain an effective amount of a polynucleotide together with a suitable amount of an aqueous solution in order to prepare pharmaceutically acceptable compositions suitable for administration to a vertebrate.

EXAMPLES

Materials and Methods

The following materials and methods apply generally to all the examples disclosed herein. Specific materials and methods are disclosed in each example, as necessary.

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The practice of the present invention will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology (including PCR), vaccinology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See, for example, *Molecular Cloning A Laboratory Manual*, 2nd Ed., Sambrook *et al.*, ed., Cold Spring Harbor Laboratory Press: (1989); *DNA Cloning*, Volumes I and II (D. N. Glover ed., 1985); *Oligonucleotide Synthesis* (M. J. Gait ed., 1984); Mullis *et al.* U.S. Pat. No: 4,683,195; *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); *Culture Of Animal Cells* (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); *Methods In Enzymology*, Vols. 154 and 155 (Wu *et al.* eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); and in Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley and Sons, Baltimore, Maryland (1989).

Plasmid Vector

Constructs of the present invention were inserted into eukaryotic expression vector V1012. This vector is built on a modified pUC18 background (*see Yanisch-Perron, C., et al. Gene 33:103-119 (1985)*), and contains a kanamycin resistance gene, the human cytomegalovirus immediate early 1 promoter/enhancer and intron A, and the bovine growth hormone transcription termination signal, and a polylinker for inserting foreign genes. See Hartikka, J., *et al., Hum. Gene Ther. 7:1205-1217 (1996)*. However, other standard commercially available eukaryotic expression vectors may be used in the present invention, including, but not limited to: plasmids pcDNA3,

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pCMV/Zeo, pCR3.1, pEF1/His, pIND/GS, pRc/CMV2, pSV40/Zeo2, pTRACER-CMV, pUB6/V5-His, pVAX1, and pZeoSV2 (available from Invitrogen, San Diego, CA), and plasmid pCI (available from Promega, Madison, WI).

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Plasmid DNA purification

Plasmid DNA was transformed into *Escherichia coli* DH5 α competent cells and highly purified covalently closed circular plasmid DNA was isolated by a modified lysis procedure (Horn, N.A., *et al.*, *Hum. Gene Ther.* 6:565-573 (1995)) followed by standard double CsCl-ethidium bromide gradient ultracentrifugation (Sambrook, J., *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press, Plainview, New York (1989)). Alternatively, plasmid DNAs are purified using Giga columns from Qiagen (Valencia, CA) according to the kit instructions. All plasmid preparations were free of detectable chromosomal DNA, RNA and protein impurities based on gel analysis and the bicinchoninic protein assay (Pierce Chem. Co., Rockford IL). Endotoxin levels were measured using *Limulus* Amebocyte Lysate assay (LAL, Associates of Cape Cod, Falmouth, MA) and were less than 0.6 Endotoxin Units/mg of plasmid DNA. The spectrophotometric A₂₆₀/A₂₈₀ ratios of the DNA solutions were typically above 1.8. Plasmids were ethanol precipitated and resuspended in an appropriate solution, *e.g.*, 150 mM sodium phosphate (for other appropriate excipients and auxiliary agents, see U.S. Patent Application Publication 20020019358, published February 14, 2002). DNA was stored at -20°C until use. DNA was diluted by mixing it with 300 mM salt solutions and by adding appropriate amount of USP water to obtain 1 mg/ml plasmid DNA in the desired salt at the desired molar concentration.

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5 Injections of plasmid DNA

 The quadriceps muscles of restrained awake mice (*e.g.*, female 6 - 12 week old BALB/c mice from Harlan Sprague Dawley, Indianapolis, IN) are injected bilaterally with 50 µg of DNA in 50 µl solution (100 µg in 100 µl total per mouse) using a disposable sterile, plastic insulin syringe and 28G 1/2 needle (Becton-Dickinson, Franklin Lakes, NJ, Cat. No. 329430) fitted with a plastic collar cut from a micropipette tip, all as previously described (Hartikka, J., *et al.*, *Hum. Gene Ther.* 7:1205-1217 (1996)).

10 Animal care throughout the study was in compliance with the "Guide for the Use and Care of Laboratory Animals", Institute of Laboratory Animal Resources, Commission on Life Sciences, National Research Council, National Academy Press, Washington, D.C., 1996 as well as with Vical's Institutional Animal Care and Use Committee.

15 Immune Correlates

 Since anthrax challenge experiments must be carried under strict containment conditions, they can be difficult and expensive, even in laboratory animals. Accordingly, it has been very important for workers in this area to develop *in vitro* assays to measure levels of immunity and to demonstrate that these assays sufficiently correlate to *in vivo* challenges. A number of *in vitro* assays, which are known to those of ordinary skill in the art to be correlates for challenges have been have been developed. See, *e.g.*, Reuveny, S. *et al. Infect. Immun.* 69:2888-2893 (2001); Kobilier, D. *et al. Infect. Immun.* 70:544-560 (2002); Pitt, M.L. *et al. Vaccine* 19:4768-4773 (2001); and Park, S., and Leppla, S.H. *Protein Expr. Purif.* 18:293-302 (2000), each of which is incorporated herein by reference in its entirety. An additional assay is described in Example 9(b), *infra*.

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EXAMPLE 1

Construction of an Isolated Polynucleotide Comprising a Human Codon-Optimized PA Coding Region, Encoding the Full Length *Bacillus Anthracis* Protective Antigen (PA)

5 A representative native *Bacillus anthracis* protective antigen (PA) nucleotide sequence consists of nucleotides 1804 to 4098 of GenBank accession number M22589 version M22589.1 GI:143280 (SEQ ID NO:3). See Welkos, S.L. *et al. Gene* 69:287-300 (1988), which is incorporated herein by reference in its entirety. The PA sequence encodes a 764 amino acid (aa) precursor protein (SEQ ID NO:4) that is processed by a signal peptidase upon
10 secretion by the bacteria, and also by host serum proteases (reviewed in Mesnage S., and Fouet, A. *J. Bacteriol.* 184:331-334 (2002), which is incorporated by reference herein in its entirety). The first 29 amino acids of PA encodes a bacterial signal sequence that is cleaved during secretion from
15 the bacteria. In the host, furin-like serum proteases cleave off the N-terminal 258 amino acids to yield PA63, the active form of PA that can bind lethal factor (LF) and edema factor (EF), thereby causing toxicity.

 A nucleic acid coding region for full-length PA (SEQ ID NO:4), optimized for human codon usage was derived by determining codon
20 frequencies from the human codon usage table (Table 2) as described above. The codon-optimized nucleic acid sequence was created by using the various codons encoding the amino acids of SEQ ID NO:4, each at the frequencies with which they occur in the codon usage table of Table 2. Although any codon-optimized coding region which encodes SEQ ID NO:4 may be used,
25 including, but not limited to SEQ ID Nos 23, 24, or 25, this Example and other Examples below use the human codon-optimized coding region encoding SEQ ID NO:4 represented by SEQ ID NO:23. Alternatively a human codon-optimized nucleic acid coding region encoding SEQ ID NO:4 can be prepared by referring to the codon usage table of Table 2, and using only the most
30 frequent codons for each amino acid, as represented by SEQ ID NO:21.

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The nucleic acid represented by SEQ ID NO:23 is constructed in the following manner. First, a series complementary oligonucleotide pairs of 80-90 nucleotides each in length and spanning the length of SEQ ID NO:23 are synthesized by standard methods. These oligonucleotide pairs are synthesized such that upon annealing, they form double stranded fragments of 80-90 base pairs, containing cohesive ends. The single-stranded ends of each pair of oligonucleotides are designed to anneal with a single-stranded end of an adjacent oligonucleotide duplex. Several adjacent oligonucleotide pairs prepared in this manner are allowed to anneal, and approximately five to six adjacent oligonucleotide duplex fragments are then allowed to anneal together via the cohesive single stranded ends. This series of annealed oligonucleotide duplex fragments is then ligated together and cloned into the TOPO® vector available from Invitrogen Corporation, Carlsbad, CA. The construct is then sequenced by standard methods. Constructs prepared in this manner, comprising 5 to 6 adjacent 80 to 90 base pair fragments ligated together, *i.e.*, fragments of about 500 base pairs, are prepared, such that the entire desired sequence of SEQ ID NO:23 is represented in a series of plasmid constructs. The inserts of these plasmids are then cut with appropriate restriction enzymes and ligated together to form the final construct. The final construct is then cloned into a standard bacterial cloning vector, and sequenced.

EXAMPLE 2

Construction of an Isolated Polynucleotide Comprising a Human Codon-Optimized LF Coding Region, Encoding the Full Length *Bacillus Anthracis* Lethal Factor (LF)

A representative native *Bacillus anthracis* lethal factor (LF) nucleotide sequence consists of nucleotides 685 to 3111 of GenBank accession number M30210 version M30210.1 GI:143141 (SEQ ID NO:11). The LF sequence encodes a 809 amino acid precursor protein that is processed to a 775 amino acid secreted protein by cleavage of its signal sequence. LF is a zinc

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metalloprotease that cleaves mitogen-activated protein kinase kinases (MAPKKs) contained inside target cells. See Mesnage S., and Fouet, A. J. *Bacteriol.* 184:331-334 (2002). Numerous mutations in LF have been described that eliminate zinc binding or the catalytic site of LF resulting in the loss of toxicity. See Hammond, S.E., and Hanna, P.C. *Infect. Immun.* 66:2374-2378 (1998). One form of inactive LF is described in detail herein, but all others could also be used with an identical approach.

A nucleic acid coding region for full-length LF (SEQ ID NO:12), optimized for human codon usage was derived by determining codon frequencies from the human codon usage table (Table 2) as described above. The codon-optimized nucleic acid sequence was created by using the various codons encoding the amino acids of SEQ ID NO:12, each at the frequencies with which they occur in the codon usage table of Table 2. Although any codon-optimized coding region which encodes SEQ ID NO:12 may be used, including, but not limited to SEQ ID NOs 26, 27, and 28, this Example and other Examples below use the human codon-optimized coding region encoding SEQ ID NO:12 represented by SEQ ID NO:26. Alternatively a human codon-optimized nucleic acid coding region encoding SEQ ID NO:12 can be prepared by referring to the codon usage table of Table 2, and using only the most frequent codons for each amino acid, as represented by SEQ ID NO:22.

The nucleic acid represented by SEQ ID NO:26 is constructed commercially by Retrogen, San Diego, CA, in the following manner. First, a series complementary oligonucleotide pairs of 80-90 nucleotides each in length and spanning the length of SEQ ID NO:26 are synthesized by standard methods. These oligonucleotide pairs are synthesized such that upon annealing, they form double stranded fragments of 80-90 base pairs, containing cohesive ends. The single-stranded ends of each pair of oligonucleotides are designed to anneal with a single-stranded end of an adjacent oligonucleotide duplex. Several adjacent oligonucleotide pairs prepared in this manner are allowed to anneal, and approximately five to six

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adjacent oligonucleotide duplex fragments are then allowed to anneal together via the cohesive single stranded ends. This series of annealed oligonucleotide duplex fragments are then ligated together and cloned into a the TOPO® vector available from Invitrogen Corporation, Carlsbad, CA. The construct is then sequenced by standard methods. Constructs prepared in this manner, comprising 5 to 6 adjacent 80 to 90 base pair fragments ligated together, *i.e.*, fragments of about 500 base pairs, are prepared, such that the entire desired sequence of SEQ ID NO:26 is represented in a series of plasmid constructs. The inserts of these plasmids are then cut with appropriate restriction enzymes and ligated together to form the final construct. The final construct is then cloned into a standard bacterial cloning vector, and sequenced.

EXAMPLE 3

Construction of Plasmid Constructs Comprising Fragments, Variants, and Derivatives of a Human Codon-Optimized Coding Region Encoding *Bacillus Anthracis* PA

Several fragments, variants, and derivatives based on SEQ ID NO:23, the human codon-optimized coding region encoding *Bacillus anthracis* PA described in Example 1, were constructed in the following manner. Codon-optimized nucleic acid fragments encoding three alternate forms of PA were constructed, namely, a nucleic acid fragment encoding full-length PA minus the furin cleavage site (PA83Δ Furin), a nucleic acid fragment encoding the active furin cleavage product of mature PA (PA63), and a nucleic acid fragment encoding the active furin cleavage product of mature PA in which Phe 342 and 343 have been deleted (PA63ΔFF). Each of these nucleic acid fragments were fused in-frame to a nucleic acid encoding a human tissue plasminogen activator (TPA) signal peptide sequence that directs the expressed PA variants and/or fragments to the secretory pathway in mammalian cells. Other useful PA fragments, variants and/or derivatives will

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be readily apparent to those of ordinary skill in the art, and are included in the present invention.

a) Construction of TPA-PA63.

5 PA63, the C-terminal fragment of PA corresponding to amino acids 199-764 of SEQ ID NO:4 corresponds to the mature, extracellularly processed protein that is able to bind to LF and edema factor (EF).

10 TPA-PA63 (Fig. 1, SEQ ID NO:1) was constructed commercially by Retrogen, San Diego, CA. A large number of other companies which provide similar construction of predetermined nucleic acid sequences are well known to those of ordinary skill in the art. The sequence was constructed in the following manner. First, a series complementary oligonucleotide pairs of 80-90 nucleotides each in length and spanning the length of SEQ ID NO:1 were synthesized by standard methods. These oligonucleotide pairs were
15 synthesized such that upon annealing, they formed double stranded fragments of 80-90 base pairs, containing cohesive ends. The single-stranded ends of each pair of oligonucleotides were designed to anneal with a single-stranded end of an adjacent oligonucleotide duplex. Several adjacent oligonucleotide pairs prepared in this manner were allowed to anneal, and approximately five
20 to six adjacent oligonucleotide duplex fragments were then allowed to anneal together via the cohesive single stranded ends. This series of annealed oligonucleotide duplex fragments were then ligated together and cloned into a the TOPO® vector available from Invitrogen Corporation, Carlsbad, CA. The construct was then sequenced by standard methods. Constructs prepared in
25 this manner, comprising 5 to 6 adjacent 80 to 90 base pair fragments ligated together, *i.e.*, fragments of about 500 base pairs, were prepared, such that the entire desired sequence of SEQ ID NO:1 was represented in a series of plasmid constructs. The inserts of these plasmids were then cut with appropriate restriction enzymes and ligated together in the TOPO® vector.

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This construct was cut with EcoRV + BamHI and the 1788 bp insert fragment (*i.e.*, SEQ ID NO:1) was cloned into the same sites of the VR1012 expression plasmid (see Hartikka *et al.*, *Hum. Gene Therapy* 7:1205-1217 (1996), which is incorporated herein by reference in its entirety). The resulting plasmid, designated VR6290, was sequenced and expressed in transiently transfected VM-92 cells in culture (see Example 6) to confirm the expression and secretion of the construct.

b) Construction of TPA-PA63ΔFF.

A different non-toxic form of PA can be generated by deleting the two phenylalanine residues at positions 342 and 343 of SEQ ID NO:4 to produce a PA protein that cannot heptamerize and form a pore to allow LF and EF to enter the cytoplasm of an infected cell. *See, e.g.*, Singh, Y. *et al. J. Biol. Chem.* 269:29039-29046 (1994), which is incorporated herein by reference in its entirety.

An expression plasmid comprising TPA-PA63Δ FF (Fig. 2, SEQ ID NO:5) was prepared by the following method. Plasmid VR6290, prepared as described in section (a), *supra*, was used as a template for PCR with the following two sets of PCR primers using Turbo *Pfu* polymerase from Stratagene Inc., La Jolla, CA

1. TPA -for 5'GAGCTTGATA TCGCCACCAT GGATGC 3' (SEQ ID NO:29) and PA del FF-Rev 5' CCACCAATAT CCGATGCATG GACTTCCGC 3' (SEQ ID NO:30) produced a 520 bp fragment.
2. HPA-endRev 5' CTTGAAGGAT CCTCAACCGA TCTCGTAG 3' (SEQ ID NO:31) and PA del FF-For 5' CCATGCATCG GATATTGGTG GCTCCGTGTC 3' (SEQ ID NO:32) produced a 1280 bp fragment that overlapped fragment 1.

Fragments 1 and 2 were gel purified using the QIAquick Gel Extraction Kit from Qiagen Inc (Valencia, CA) and the fragments were combined in a subsequent PCR reaction and amplified with the primer pair

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TPA-for and HPA-endRev to yield the full length 1782 bp fragment shown in Fig 2. This fragment was digested with the restriction enzymes EcoR5 + BamHI and ligated into the same sites of the VR1012 expression plasmid. The resulting plasmid, designated VR6291, was sequenced and expressed in transiently transfected VM-92 cells in culture (see Example 6) to confirm the expression and secretion of the construct.

c) Construction of TPA-PA83Δ Furin.

Deleting the furin cleavage site of the mature PA, *i.e.*, amino acids 192-197 (Ser-Arg-Lys-Lys-Arg-Ser) of SEQ ID NO:4, yields a protein that is secreted from the cell and that can bind the host cell receptor but cannot bind LF or EF and therefore is non-toxic. *See, e.g.*, Singh, Y. *et al. Infect. Immun.* 66:3447-3448 (1998), and Klimpel KR, *et al. Proc. Natl. Acad. Sci. USA* 89:10277-10281 (1992), which are incorporated herein by reference in their entireties.

An expression plasmid comprising TPA-PA83Δfurin (Fig. 3, SEQ ID NO:7) was constructed in the following manner. A plasmid comprising a codon-optimized nucleotide sequence (as per the sequence of SEQ ID NO:23) encoding the N-terminal 20 kD domain of PA, *i.e.*, corresponding to the portion of PA that is cleaved off by furin, was synthesized by Retrogen Inc. according to the method described in section a), *supra*. This plasmid was cut with EcoRV+AfeI and the 570 bp insert was gel purified as above. The plasmid VR6290 described in section a) above was digested with EcoRV+AfeI and the 6.6 kb linear vector fragment was gel purified and ligated to the 570 bp N-terminal fragment. Transformed colonies were screened for recombinants by PCR using the primer pair NtermPA seqF 5' GTGGACGACC AGGAAGTGAT C 3' (SEQ ID NO:33) and NtermPA seqR 5' GGCTATCTGT CCAGTACAGC TTGAA3' (SEQ ID NO:34). A selected recombinant, designated VR6292, was sequenced and was expressed in

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transiently transfected VM-92 cells in culture (see Example 6) to confirm the expression and secretion of the construct.

EXAMPLE 4

5 Construction of Plasmid Constructs Comprising Fragments, Variants, and
Derivatives of a Human Codon-Optimized Coding Region Encoding *Bacillus*
Anthracis LF

Several fragments, variants, and derivatives of SEQ ID NO:26, the human codon-optimized coding region encoding *Bacillus anthracis* LF, as prepared in Example 2, were constructed in the following manner. Codon-
10 optimized nucleic acid fragments encoding four alternate forms of LF were constructed, namely, a nucleic acid fragment encoding the full-length mature LF in which His 686, His 690 and Glu 687 have been substituted with Ala, Ala, and Asp, respectively (LF HEXXH), a nucleic acid fragment encoding amino acids 34 to 583 of full-length LF, encoding domains I-III of mature LF
15 (LF Domain I-III), a nucleic acid fragment encoding amino acids 34 to 254 of mature LF, corresponding to domain I of mature LF (LF Domain IA), and a nucleic acid fragment encoding amino acids 34 to 295 of mature LF, corresponding to domain I of mature LF (LF Domain IB). Each of these nucleic acid fragments were fused in-frame to a nucleic acid encoding a
20 human tissue plasminogen activator (TPA) signal peptide sequence that directs the expressed LF variants and/or fragments to the secretory pathway in mammalian cells. Furthermore, other useful LF fragments, variants and/or derivatives would be readily apparent to those of ordinary skill in the art.

25 a) Construction of TPA-LF HEXXH.

This construct encodes full length LF (minus the bacterial signal sequence) with three point mutations that render LF non-toxic. Each of these mutations, alone or together, are thought to eliminate the enzymatic activity of LF, thereby rendering it non-toxic. See, *e.g.*, Hammond, SE and Hanna PC,

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Infect. Immun. 66:2374-2378 (1998), which is incorporated herein by reference in its entirety. Other LF mutants contained in this reference, e.g., LF^{E687C}, LF^{B687D}, LF^{H686A}, LF^{H690A}, and LF^{H686A+H690A}, are also included in the present invention. While not being bound by theory, substitution of the histidine residues at positions 686 and 690 is thought to decrease zinc binding, resulting in decreased or no protease activity, and substitution of the glutamic acid at position 687 is thought to also eliminate protease activity, thereby resulting in no *in vitro* or *in vivo* macrophage killing. This construct combines all three mutations to afford a greater perceived level of safety than either point mutation alone.

An expression plasmid comprising LF HEXXH (Fig. 4, SEQ ID NO:9) was prepared in the following manner. The entire 2418 bp sequence was synthesized by Retrogen Inc. and inserted into the EcoRV and BamHI sites of the TOPO vector as described in Example 3(a). The resulting plasmid was digested with EcoRV and BamHI and the 2418 bp insert was purified by gel electrophoresis as described above. The insert was ligated into EcoRV+BamHI digested VR1012 and transformed into *E. coli*. Transformed colonies were screened for recombinants by PCR using the primer pair seqF1-hLF 5' CCGTGCTCGT TATTCAGAGT 3' (SEQ ID NO:35) and seqR2-hLF 5' CCTTCTCTTC TGTGCTAAGG 3' (SEQ ID NO:36). A selected recombinant, designated VR6295, was sequenced and was expressed in transiently transfected VM-92 cells in culture (see Example 6) to confirm the expression and secretion of the construct.

b) Construction of TPA-LF Domain I-III.

This construct encodes the N-terminal amino acids 34-583 of mature LF, corresponding to domains I-III. The entire protease domain (domain IV) has been deleted and is therefore non-toxic. See, e.g., Pannifer AD *et al.* *Nature* 414:229-233 (2001), which is incorporated herein by reference in its entirety.

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Recent data suggest LF is capable of entering cells independently of PA using a region at the N terminal domain (Kushner, N. *et al. Proc. Natl. Acad. Sci.* 100: 6652-7 (2003)). In addition, the full length LF is able to cause impairment of dendritic cell function via domain IV protease degradation of MAP activated protein kinase kinase (MAPKK). Agrawal, A. *et al. Nature* 424: 329-34 (2003)). Therefore LF, independently of its association with PA, may have toxic effects which could be blocked through vaccination. Through the inclusion of an LF component in the vaccine of the present invention, it may be possible to neutralize LF at a number of domains and to block potential toxicities that occur in conjunction with, or independent of, binding to PA. In may also be possible to block the primary binding of LF to PA.

An expression plasmid comprising TPA-LF Domain I-III (Fig. 5, SEQ ID NO:13) was prepared in the following manner. The plasmid VR6295 (as produced in section a) above, was PCR amplified with the primer pair TPA-for (SEQ ID NO:29) and LF-DomII-R 5' GAACCTGGAT CCCTACACCA CCTTGGCGTC GATG 3' (SEQ ID NO:37) using *Pfu* polymerase. The 1740 bp fragment was gel purified, digested with EcoRV + BamHI and cloned into VR1012. Transformed colonies were screened by PCR using the same amplification primers. A selected recombinant, designated VR62952, was sequenced and was expressed in transiently transfected VM-92 cells in culture (see Example 6) to confirm the expression and secretion of the construct.

c) Construction of TPA-LF Domain IA.

This construct encodes the N-terminal amino acids 34-254 of mature LF, corresponding generally to domain I. This is the portion of LF that directly binds PA. See, e.g., Pannifer AD *et al. Nature* 414:229-233 (2001).

An expression plasmid comprising TPA-LF Domain I (Fig. 6, SEQ ID NO:15) was prepared in the following manner. The plasmid VR6295 (as produced in section a) above, was PCR amplified with the primer pair TPA-for (SEQ ID NO:29) and G-LF-R 5'GCTAATGGAT CCTCAAAATG

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CCTTGGCGAA CACCT 3' (SEQ ID NO:38) using *Pfu* polymerase. The 753 bp fragment was gel purified, digested with EcoRV + BamHI and cloned into VR1012. Transformed colonies were screened by PCR using the same amplification primers. A selected recombinant, designated VR6295G, was sequenced and was expressed in transiently transfected VM-92 cells in culture (see Example 6) to confirm the expression and secretion of the construct.

d) Construction of TPA-LF Domain IB.

This construct encodes the N-terminal amino acids 34-295 of mature LF, also corresponding generally to domain I.

An expression plasmid comprising TPA-LF Domain IB (Fig. 14, SEQ ID NO:39) was prepared in the following manner. The plasmid VR6295 (as produced in section a) above, was PCR amplified with the primer pair TPA-for (SEQ ID NO:29) and crystal-LF-R 5' CCATACGGAT CCTCACTGGT CTTTCAGTTC CTCCA 3' (SEQ ID NO:41) using *Pfu* polymerase. The 876 bp fragment was gel purified, digested with EcoRV + BamHI and cloned into VR1012. Transformed colonies were screened by PCR using the same amplification primers. A selected recombinant, designated VR62951, was sequenced and was expressed in transiently transfected VM-92 cells in culture (see Example 6) to confirm the expression and secretion of the construct.

EXAMPLE 5

N-Linked Glycosylation Mutants

Most mammalian transmembrane and secreted proteins are glycosylated post-translationally in the endoplasmic reticulum. See, e.g., Lodish H *et al.* Molecular Cell Biology 4th edition, W. H. Freeman and Company, New York. There are two main types of protein glycosylation in mammalian cells, N-linked and O-linked. N-linked glycosylation occurs on asparagine (N) residues at the amino acid motif N-X-(S/T) where X refers to

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any amino acid residue and S/T denotes serine or threonine. There are seven N-linked glycosylation motifs in mature LF, twelve N-linked glycosylation motifs in full-length mature PA (PA83) and ten N-linked glycosylation motifs in PA63. Since this glycosylation does not occur in bacteria, the anthrax antigens synthesized in mammalian cells after DNA immunization may differ from the PA and LF in anthrax toxin secreted by *B. anthracis*. See, e.g., Schaffer C. *et al. Proteomics* 1:248-246 (2001), which is incorporated herein by reference in its entirety. This mammalian N-linked glycosylation could obscure or alter B-cell antibody epitopes that are normally exposed in conventional anthrax protein vaccines. Therefore codon-optimized coding regions encoding PA63 and LF were made in which the asparagines in the N-linked glycosylation motifs (N-X-S/T) motifs were mutated to glutamines (Q-X-S/T). The motif Q-X-S/T is not subject to glycosylation in mammals. Such "sugar minus" variants of any of the variants, fragments, derivatives, or full length coding regions disclosed herein, as well as addition variants, fragments and derivatives known to those of skill in the art are encompassed by the present invention.

All asparagine (N) residues in the N-X-S/T motifs contained in TPA-PA63 (SEQ ID NO:1, produced as described in Example 3(a)) and TPA-LFAHEXXH (SEQ ID NO:9, produced as described in Example 4(a)) were mutated to Glutamine (Q) by generating a series of overlapping PCR fragments. As described in more detail below, these fragments were added together two at a time and amplified with primers at the extreme end of the two fragments to build larger and larger PCR fragments until a full length mutant was obtained. In each case, the full-length fragment was gel purified, digested with EcoRV + BamHI and cloned into VR1012. All PCR reactions were performed with *Pfu* polymerase from Stratagene Inc using standard conditions.

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a) Construction of TPA-sugar minus PA63.

This construct is the same as SEQ ID NO:1, except that all ten N-X-S/T motifs in the encoded polypeptide have been changed to Q-X-S/T, via point mutations. The mutated construct was assembled from overlapping PCR fragments using SEQ ID NO:1 as the template.

Ten nanograms quantities of plasmid VR6290 DNA was amplified with each of the 10 primer pairs listed in Table 8. The fourth column lists the size of the resulting PCR products with the various primer pairs. Each of these resulting PCR fragments has a single stranded region at each end, which can anneal with a single stranded region on another of the fragments.

TABLE 8

PCR Fragment	Forward Primer	Reverse Primer	Size
1	TPA-For (SEQ ID NO:29)	PA-R1 (SEQ ID NO:42)	310 bp
2	PA-F2 (SEQ ID NO:43)	PA-R2 (SEQ ID NO:44)	140 bp
3	PA-F3 (SEQ ID NO:45)	PA-R3 (SEQ ID NO:46)	90 bp
4	PA-F4 (SEQ ID NO:47)	PA-R4 (SEQ ID NO:48)	180 bp
5	PA-F5 (SEQ ID NO:49)	PA-R5 (SEQ ID NO:50)	260 bp
6	PA-F6 (SEQ ID NO:51)	PA-R6 (SEQ ID NO:52)	100 bp
7	PA-F7 (SEQ ID NO:53)	PA-R7 (SEQ ID NO:54)	185 bp
8	PA-F8 (SEQ ID NO:55)	PA-R8 (SEQ ID NO:56)	150 bp
9	PA-F9 (SEQ ID NO:57)	PA-R9 (SEQ ID NO:58)	130 bp
10	PA-F10 (SEQ ID NO:59)	PA-R10 (SEQ ID NO:60)	135 bp
11	PA-F11 (SEQ ID NO:61)	HPA-endRev (SEQ ID NO:31)	80 bp

2.5 microliters of each PCR fragment in Table 8 was combined pairwise with a second PCR fragment in Table 8. The two fragments were allowed to anneal and were used as templates in a second series of PCR reactions, with resulting PCR fragments as shown in Table 9.

TABLE 9

PCR Fragment	Template Fragments	Forward Primer	Reverse Primer	Size
12	2 + 3	PA-F2 (SEQ ID NO:43)	PA-R3 (SEQ ID NO:46)	230 bp
13	4 + 5	PA-F4 (SEQ ID NO:47)	PA-R5 (SEQ ID NO:50)	440 bp
14	6 + 7	PA-F6 (SEQ ID NO:51)	PA-R7 (SEQ ID NO:54)	285 bp
15	8 + 9	PA-F8 (SEQ ID NO:55)	PA-R9 (SEQ ID NO:58)	280 bp
16	10 + 11	PA-F10 (SEQ ID NO:59)	HPA-endRev (SEQ ID NO:31)	215 bp

2.5 microliters of each PCR fragment in Table 9 was combined pair wise with a second PCR fragment in Table 9. The two fragments were allowed to anneal and were used as templates in a third series of PCR reactions, with resulting PCR fragments as shown in Table 10.

TABLE 10

PCR Fragment	Template Fragments	Forward Primer	Reverse Primer	Size
17	1 + 12	TPA-For (SEQ ID NO:29)	PA-R3 (SEQ ID NO:46)	540 bp
18	13 + 14	PA-F4 (SEQ ID NO:47)	PA-R7 (SEQ ID NO:54)	725 bp
19	15 + 16	PA-F8 (SEQ ID NO:55)	HPA-endRev (SEQ ID NO:31)	495 bp

Fragments 17, 18, and 19 were gel purified before proceeding to the next series of PCR reactions. The last two sets of PCR reactions were carried out as listed in Table 11, using 2.5 microliters of the annealed PCR fragment pairs listed in the second column, which had been gel purified.

TABLE 11

PCR Fragment	Template Fragments	Forward Primer	Reverse Primer	Size
20	17 + 18	TPA-For (SEQ ID NO:29)	PA-R7 (SEQ ID NO:54)	1265 bp
21	19 + 20	TPA-For (SEQ ID NO:29)	HPA-endRev (SEQ ID NO:31)	1788 bp

Resulting PCR fragment 21 represents the full-length TPA-Sugar minus PA63 fragment (Figure 7, SEQ ID NO:17). The TPA-sugar minus PA63 fragment was cloned into the VR1012 expression plasmid. A selected recombinant, designated VR6299, was sequenced, and was expressed in

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transiently transfected VM-92 cells in culture (see Example 6) to confirm the expression and secretion of the construct.

The sequences of the primers used in the PCR reactions in this Example are listed in Table 12.

5

TABLE 12

SEQ ID NO:	Primer	Sequence
29	TPA -for	GAGCTTGATATCGCCACCATGGATGC
42	PA-R1	CTGGAGACACCTGTTTATCGATCC
43	PA-F2	GGATCGATAAACAGGTGTCTCCAG
44	PA-R2	GAAGTACTGGTCTGTTTAGATATGGT
45	PA-F3	ACCATATCTAAACAGACCAGTACTTC
46	PA-R3	CGTCGAGGACTGGCTATTGCTAA
47	PA-F4	TTAGCAATAGCCAGTCCTCGACG
48	PA-R4	GAGGGTCTGCTGTTTGCCCAGG
49	PA-F5	CCTGGGCAAACAGCAGACCCTC
50	PA-R5	CTTCAGACCACTGTGACCCAGTG
51	PA-F6	CACTGGGTACAGTGGTCTGAAG
52	PA-R6	GATCACTGGGCTGCACGGCGG
53	PA-F7	CCGCCGTGCAGCCCAGTGATC
54	PA-R7	TATTGGTGGCCTGCAGCTCTGC
55	PA-F8	GCAGAGCTGCAGGCCACCAATA
56	PA-R8	CAGTACTGCTCTGGATAACTTCCC
57	PA-F9	GGGAAGTTATCCAGAGCAGTACTG
58	PA-R9	AAGCTGGAAATCTGCAGCATATCAT
59	PA-F10	ATGATATGCTGCAGATTTCAGCTT
60	PA-R10	CTCGCTTGGCTGGATGATTGTGT
61	PA-F11	ACACAATCATCCAGCCAAGCGAG
31	HPA-endRev	CTTGAAGGATCCTCAACCGATCTCGTAG

b) Construction of TPA-sugar minus LF HEXXH.

This construct is the same as SEQ ID NO:9, except that all seven N-X-S/T motifs in the encoded polypeptide have been changed to Q-X-S/T, via point mutations. The mutated construct was assembled from overlapping PCR fragments using standard methods, using primers which code for Q residues instead of N residues in the seven glycosylation motifs, and using SEQ ID NO:9 as the template.

10

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Ten nanograms quantities of plasmidVR6295 DNA was amplified with each of the 8 primer pairs listed in Table 13. The fourth column lists the size of the resulting PCR products with the various primer pairs. Each of these resulting PCR fragments has a single stranded region at each end, which can

5

TABLE 13

PCR Fragment	Forward Primer	Reverse Primer	Size
1	TPA-For (SEQ ID NO:29)	LF-R1 (SEQ ID NO:62)	170 bp
2	LF-F2 (SEQ ID NO:63)	LF -R2 (SEQ ID NO:64)	450 bp
3	LF -F3 (SEQ ID NO:65)	LF -R3 (SEQ ID NO:66)	220 bp
4	LF -F4 (SEQ ID NO:67)	LF -R4 (SEQ ID NO:68)	580 bp
5	LF -F5 (SEQ ID NO:69)	LF -R5 (SEQ ID NO:70)	700 bp
6	LF -F6 (SEQ ID NO:71)	LF -R6 (SEQ ID NO:72)	70 bp
7	LF -F7 (SEQ ID NO:73)	LF -R7 (SEQ ID NO:74)	65 bp
8	LF -F8 (SEQ ID NO:75)	HLFend-R (SEQ ID NO:76)	165 bp

2.5 microliters of each PCR fragment in Table 13 was combined pair wise with a second PCR fragment in Table 13. The two fragments were allowed to anneal and were used as templates in a second series of PCR reactions, with resulting PCR fragments as shown in Table 14.

10

TABLE 14

PCR Fragment	Template Fragments	Forward Primer	Reverse Primer	Size
9	1 + 2	TPA-For (SEQ ID NO:29)	LF -R2 (SEQ ID NO:64)	620 bp
10	3 + 4	LF-F3 (SEQ ID NO:65)	LF-R4 (SEQ ID NO:68)	800 bp
11	5 + 6	LF-F5 (SEQ ID NO:69)	LF-R6 (SEQ ID NO:72)	770 bp
12	7 + 8	LF-F7 (SEQ ID NO:73)	HLFend-R (SEQ ID NO:76)	230 bp

2.5 microliters of each PCR fragment in Table 14 was combined pair wise with a second PCR fragment in Table 14. The two fragments were allowed to anneal and were used as templates in a third series of PCR reactions, with resulting PCR fragments as shown in Table 15.

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TABLE 15

PCR Fragment	Template Fragments	Forward Primer	Reverse Primer	Size
13	9 + 10	TPA-For (SEQ ID NO:29)	LF-R4 (SEQ ID NO:68)	1420 bp
14	11 + 12	LF-F5 (SEQ ID NO:69)	HLFend-R (SEQ ID NO:76)	1000 bp

Fragments 13 and 14 were gel purified before proceeding to the final PCR reaction. This PCR reaction was carried out as listed in Table 16, using 2.5 microliters of the annealed PCR fragment pairs listed in the second column, which had been gel purified.

TABLE 16

PCR Fragment	Template Fragments	Forward Primer	Reverse Primer	Size
15	13 + 14	TPA-For (SEQ ID NO:29)	HLFend-R (SEQ ID NO:76)	2418 bp

Resulting PCR fragment 15 represents the full-length TPA-Sugar minus LF HEXXH fragment (Figure 8, SEQ ID NO:19). The TPA-sugar minus LF HEXXH fragment was cloned into the VR1012 expression plasmid. A selected recombinant, designated VR6300, was sequenced and was expressed in transiently transfected VM-92 cells in culture (see Example 6) to confirm the expression and secretion of the construct.

The sequences of the primers used in the PCR reactions in this Example are listed in Table 17.

TABLE 17

SEQ ID NO:	Primer	Sequence
29	TPA -for	GAGCTTGATATCGCCACCATGGATGC
62	LF-R1	TCCTGTGTTTTCTGACGTTCTTCG
63	LF-F2	CGAAGAACGTCAGAAAACACAGGA
64	LF-R2	TATCTGACGCCTGTTTGATTGTGTT
65	LF-F3	AACACAATCAAACAGGCGTCAGATA
66	LF-R3	CCAGAGACAGCTGAATCTCCTGTT
67	LF-F4	AACAGGAGATTGAGCTGTCTCTGG
68	LF-R4	AGCGGTGAGCTGGTTAATATTCATG

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SEQ ID NO:	Primer	Sequence
69	LF-F5	CATGAATATTAACCAGCTCACCGCT
70	LF-R5	CCTCAGAATCCTGTCGAAGCTCA
71	LF-F6	TGAGCTTCGACAGGATTCTGAGG
72	LF-R6	GATCAGACTGCTGCTTATCCAACA
73	LF-F7	TGTTGGATAAGCAGCAGTCTGATC
74	LF-R7	AGGAAGTCAGCTGACTCCCTTCC
75	LF-F8	GGAAGGGAGTCAGCTGACTTCCT
76	HLFend-R	GCAGATCTGGATCCTCAAGAG

EXAMPLE 6

In vitro Expression of Human Codon-Optimized Coding Regions Encoding *B. Anthracis* PA and LF, and Fragments, Variants and Derivatives thereof, in a Murine Cell Line

The expression plasmids described Examples 3-5 above and the corresponding wild type *Bacillus anthracis* genes were initially analyzed in *in vitro* transiently transfected cells in culture. Initial studies were carried out in a well characterized mouse melanoma cell line (VM-92, also known as UM-449), using cationic lipid-based transfection procedures well known to those of skill in the art. Other standard cell lines, for example, COS-1 cells, COS -7 cells, CHO cells, HEK-293 cells, and HeLa cells, may be used for transient transfections as well. Following transfection, cell lysates and culture supernatants of transfected cells were evaluated to compare relative levels of expression of *B. anthracis* antigen proteins. The samples were assayed by western blots and ELISAs, using commercially available anti-PA and Anti-LF monoclonal antibodies (available from Research Diagnostics Inc., Flanders NJ), so as to compare both the quality and the quantity of expressed antigen. Additionally, *in vitro* transfection assays were used to determine the effect of mixing the various plasmids comprising codon-optimized coding regions encoding non-toxic PA and LF on levels of expression in mammalian cells.

Expression products derived from cells transfected with the various polynucleotide constructs are examined to ensure the correct or predicted

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molecular weight of the recombinant antigens, and immunoreactivity of the recombinant antigens (*i.e.*, to react with *B. anthracis* antisera). In addition, a comparison of expression levels (both intra- and extra-cellular) of each class of expression plasmid (*e.g.*, wild type vs. human codon-optimized; truncated vs. full-length) is made.

EXAMPLE 7

In vitro Expression of Human Codon-Optimized Coding Regions Encoding *B. Anthracis* PA and LF, and Fragments, Variants and Derivatives Thereof, in a Human Cell Line

The expression plasmids described Examples 3-5 above and the corresponding wild type *Bacillus anthracis* genes are also analyzed in *in vitro* transfected human cells in culture. These studies are carried out in a well characterized human cell line, *e.g.*, HeLa cells, ATCC Accession No. CCL-2, available from the American Type Culture Collection, Manassas, VA, using cationic lipid-based transfection procedures well known to those of skill in the art. Following transfection, cell lysates and culture supernatants of transfected cells are evaluated to compare relative levels of expression of *B. anthracis* antigen proteins. The samples are assayed by western blots and ELISAs, using commercially available antiPA and Anti-LF monoclonal antibodies (available from Research Diagnostics Inc., Flanders NJ), so as to compare both the quality and the quantity of expressed antigen. Additionally, *in vitro* transfection assays are used to determine the effect of mixing the various plasmids comprising codon-optimized coding regions encoding non-toxic PA and LF on levels of expression in human cells.

Expression products from the derived from human cells transfected with the various polynucleotide constructs are examined for molecular weight, and expression immunoreactive antigens (*i.e.*, to react with *B. anthracis* antisera). In addition, a comparison of expression levels (both intra- and

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extra-cellular) of each class of expression plasmid (e.g., wild type vs. human codon-optimized; truncated vs. full-length) is made.

EXAMPLE 8

Animal Immunization and Challenge

5 The immunogenicity of expression products encoded by the codon-optimized polynucleotides described in Examples 1-5 are evaluated based on each plasmid's ability to mount a humoral immune response *in vivo*. Plasmids are tested individually and in combinations by injecting single constructs as well as multiple constructs in various animals as described below.
10 Immunizations are initially carried out in mice by intramuscular (IM) injections. Serum is collected from immunized animals, and the immune response is quantitated by ELISA assay using commercially available antiPA and Anti-LF monoclonal antibodies (available from Research Diagnostics Inc., Flanders NJ) according to standard protocols. The tests of immunogenicity
15 further include measuring antibody titer, neutralizing antibody titer, and challenging immunized animals with toxin protein.

 Testing in rabbits are then used to confirm the results in mice and thereby provide efficacy data for the best plasmids in more than one mammalian immunogenicity model system. Serum is collected from
20 immunized rabbits, and antibody titers and neutralizing antibody titers are determined. In addition, immunized rabbits are tested with a spore inhalation challenge. The combined results determine the plasmids to be subsequently tested in non-human primates.

25 a) Mouse immunizations.

 The plasmid constructs described in Examples 3-5, as well as similar plasmid constructs comprising native coding regions encoding native PA and LF, as well as empty control plasmids, are tested *in vivo* in mice by

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intramuscular injection of the rectus femoris muscle within the quadriceps, using methods described above. There are 5-10 animals per group. A standard DNA vaccination protocol is used (50 µg DNA in 150 mM sodium phosphate (1 mg/ml)/leg at 0, 14 and 28 days). Alternative DNA formulations include PBS instead of sodium phosphate, adjuvants, *e.g.*, Vaxfectin™ at a 4:1 DNA: Vaxfectin™ mass ratio, mono-phosphoryl lipid A (detoxified endotoxin) from *S. minnesota* (MPL) and trehalosedicorynomycolateAF (TDM), in 2% oil (squalene)-Tween 80-water (MPL + TDM, available from Sigma/Aldrich, St. Louis, MO, (catalog # M6536)), a solubilized mono-phosphoryl lipid A formulation (AF, available from Corixa), (±)-N-(3-Acetoxypropyl)-N,N-dimethyl-2,3-bis(octyloxy)-1-propanaminium chloride (compound # VC1240), or poloxamers, *e.g.*, CRL1005 (from Organichem) and a solution of benzyl-alkonium chloride "BAK" (from Ruger Chemicals)("CRL 1005/BAK") (*see* Shriver, J.W. *et al.*, *Nature* 415:331-335 (2002), and P.C.T. Publication No. WO 02/00844 A2, each of which is incorporated herein by reference in its entirety); or transfection-facilitating cationic lipids, *e.g.*, DMRIE/DOPE at a 4:1 DNA:lipid mass ratio.

Serum samples for antibody assays are taken at 0, 21, and 41 days. On or about day 42, the vaccinated animals are challenged using either a tail vein injection of purified lethal factor toxin (Letx) or pulmonary delivery of aerosolized *B. anthracis*. Mice are challenged using the purified *B. anthracis* lethal toxin (Letx), *i.e.*, the combined mature PA65 and LF proteins. These proteins are provided through a collaborative agreement with Dr. Stephen Leppla, National Institutes of Dental Research, at the NIH. The proteins are expressed in *E.coli* as recombinant proteins and purified according to published protocols (*see, e.g.*, Leppla, *SH Methods Enzymol.* 165:103-116 (1988) and Park, S and Leppla, *SH Protein Expr. Purif.* 18:293-302 (2000), each of which are incorporated herein by reference in their entireties). The challenge is conducted by injecting the mouse tail vein with a protein cocktail containing 60 µg of purified PA and 25-30 µg of purified LF. This

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approximates the equivalent of five 50% lethal doses of Letx. The animals are monitored for morbidity and mortality at regular intervals following challenge.

b) Rabbit immunizations.

5 The rabbit has increasingly gained acceptance as a relevant animal model to evaluate efficacy of vaccines against *B. anthracis*. The plasmid constructs described in Examples 3-5, as well as similar plasmid constructs comprising native coding regions encoding native PA and LF, as well as empty control plasmids, are tested *in vivo* in rabbits by the following method.

10 Plasmid vaccination of rabbits is done at four-week intervals. At each time point, the animals (n=2-4) receive an IM injection (quadriceps) of 500 µg (1mg/ml) of DNA in 150 mM sodium phosphate formulated with the adjuvant Vaxfectin™ at a 4:1 DNA:Vaxfectin™ mass ratio, each animal receiving a total of 3 injections (1500 µg/animal). Alternative DNA formulations include

15 other adjuvants as described herein, for example, CRL1005/BAK (*see* Shriver, J.W. *et al.*, *Nature* 415:331-335 (2002), and P.C.T. Publication No. WO 02/00844 A2), and/or transfection-facilitating cationic lipids, *e.g.*, DMRIE/DOPE at a 4:1 DNA:lipid mass ratio. Serum samples are taken at

20 Day 0, 42, and 69 to determine antibody titers. The animals receive an aerosolized challenge on Day 70.

 Rabbits are challenged in a BSL-3 facility (available, for example, at the Battelle Medical Research Evaluation Facility (MREF) in West Jefferson, OH) by standard methods. See, *e.g.*, Henderson, DW *J. Hygiene* 50:53-68 (1952)). The Battelle facility has the equipment, staff, and certification to

25 safely conduct a aerosol challenge of large mammals using infectious and toxin producing *B. anthracis*. Vaccinated animals are transferred to Battelle's facility in West Jefferson, and then, after a IACUC approved holding isolation period, the animals are challenged with between 50 and 100 LD50 aerosolized *B. anthracis* spores by inhalation. The animals are monitored for morbidity

30 and mortality at regular intervals following challenge.

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c) Non-human primate immunizations.

The plasmid constructs described in Examples 3-5, as well as similar plasmid constructs comprising native coding regions encoding native PA and LF, as well as empty control plasmids, are tested *in vivo* in non-human primates by the following method. Cynomolgus macaques (*M. fascicularis*) are used for immunization and challenge experiments. Plasmid vaccination of the macaques is done at four-week intervals. Animals receive 1 to 1.5 mg each of DNA at each immunization bilaterally (2 to 3 mg total) intramuscularly, in the deltoid muscle. Following immunization, all animals are challenged by pulmonary delivery of aerosolized *B. anthracis*.

d) Human immunizations.

The plasmid constructs described in Examples 3-5, as well as similar plasmid constructs comprising native coding regions encoding native PA and LF, as well as empty control plasmids, are tested *in vivo* in healthy human volunteers by the following method. The plasmids are formulated in 150 mM sodium phosphate, optionally including Vaxfectin™ at a 4:1 DNA: Vaxfectin™ mass ratio, and or a poloxamer, *e.g.*, 0.01% (w/v) Pluronic® R 25R2. Vaccinations are given at 0, 4, and 8 weeks intramuscularly into the deltoid muscle either by needle injection or by needleless Biojector jet (*see, e.g., Wang, R. et al. Proc. Natl. Acad. Sci. USA 98:10817-10822 (2001)*). The volunteers receive 1 to 1.5 mg each of DNA at each immunization. Following immunization, serum specimens are collected from the volunteers and tested for antibodies to *B. anthracis* LF or PA.

e) Laboratory animal, companion animal, or food animal immunizations.

Plasmid constructs such as those described in Examples 3-5, are prepared using codon-optimized coding regions optimized for the species of

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interest using an appropriate codon-usage table, e.g., Table 3 (mouse), Table 4 (domestic cat), or Table 5 (cow). Codon optimization may be carried out by using relative frequencies for the codons, or by using the most frequent codon, as described herein. Plasmids comprising these coding regions, plus similar plasmid constructs comprising native coding regions encoding native PA and LF, as well as empty control plasmids, are tested *in vivo* in various animal species by the following method. The animal species of interest is immunized with an appropriate amount of a DNA vaccine codon-optimized for that species, at an appropriate amount, delivered in an appropriate route for that species, including, but not limited to the following immunization strategies: for mouse immunization, intramuscular delivery into the rectus femoris muscle of 50 µg DNA in 150 mM sodium phosphate (1 mg/ml)/leg at 0, 14 and 28 days; for cow immunization, intradermal delivery into the ear of 500 µg DNA in normal saline (1 mg/ml) at days 0 and 21 (*see, e.g., van Drunen Little-van den Hurk et al. J. Gen. Virol. 79:831-839 (1998)*); and for domestic cat immunization, intradermal delivery of 300 µg DNA in normal saline (1 mg/ml) at days 0, 15, and 30 (*see, e.g., Osorio, JE, et al. Vaccine 17:1109-1116 (1999)*).

EXAMPLE 9

Immunological Assays

a) ELISA for LF and PA Antibody Titers.

Microtiter plates are coated with either PA or LF antigen by incubating 100 ng/well of purified protein (obtained from List Biological Laboratories, Campbell, CA) overnight at 4°C in 100 mM carbonate buffer, pH 9.6. The wells are washed (3X) with 10 mM Tris-buffered (pH 7.3); 150 mM NaCl (TBS) followed by a 1% (w/v) BSA block. Serially diluted experimental and control serum samples in TBS + 0.05% Tween are added to the wells and incubated for 60 min at room temperature. Enzyme conjugated (horseradish

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peroxidase or alkaline phosphatase) anti-mouse, anti-rabbit, or anti-monkey IgG are then added to each well and supernatants monitored for enzyme product. Antibody titers are defined as the highest dilution of a serum sample that results in an absorbance value 2X greater than that of a non-immune control serum. Antibody quantification will be determined using a purified anti-PA and anti-LF IgG1 and IgG2 reagent antibody.

b) Toxin Neutralization Assay.

Antibodies from vaccinated animals are initially tested using an *in vitro* assay that measures the neutralization of lethal toxin (Letx, *i.e.*, LF and PA protein) cytotoxicity. Briefly, this protection assay is carried out using 24 hr. cultures of J774A.1 mouse macrophage cells maintained in microtiter plates ($\sim 6 \times 10^4$ cells per well) in DME media, with glucose and L glutamine supplements, and 7% fetal bovine serum at 37°C. Serially diluted serum from vaccinated and control animals are mixed with letx and allowed to sit for 60 min. The final Letx concentration will be brought to 3 µg/ml. This mixture will then added to the J774A.1 cells and incubated for seven hours at 37°C. Finally, 100 µl of 0.5 mg/ml 3-[4,5-dimethylthiazol-2yl]-2,5-diphenyltetrazolium bromide (MTT) is added to each experimental well and allowed to incubate another 60 min. before assaying for cytotoxicity. In this assay, surviving cells metabolize MTT into an insoluble purple pigment in a manner that is proportional to viability. This insoluble pigment is recovered from viable cells and quantitated by absorption of 450nm light.

EXAMPLE 10

Immunization using a Prime-Boost Strategy

There is accumulating evidence to suggest that a naked DNA prime with a heterologous viral or protein boost will result in an enhanced humoral response. Since the humoral response is widely believed to be the immune

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correlate of protection against *B. anthracis*, in certain experiments a prime-boost strategy is used. The boost may be purified non-toxic LF and/or PA protein or the commercially available AVA vaccine. Alternatively recombinant virus vectors, e.g., adenovirus vectors, expressing non-toxic LF and/or PA may be used as the boost. Results are evaluated to compare antibody titers resulting from prime-boost immunization relative to DNA vaccination alone.

New Zealand rabbits are immunized with a series of three plasmid injections or two plasmid injections with the plasmid constructs described in Examples 3-5, as well as similar plasmid constructs comprising native coding regions encoding native PA and LF, as well as empty control plasmids, followed by a single dose of recombinant PA and/or LF protein (1 microgram in Alhydrogel) or the AVA vaccine (5 microliters). Controls include immunization with the codon optimized and control plasmid constructs alone, and mock immunizations. Following the immunization series, e.g., two plasmid DNA immunizations at four week intervals followed by a boost at week 12, total antibody titers and neutralizing titers are determined. In addition, selected immunized animals are challenged with a 500x LD50 dose of aerosolized anthrax spores at Battelle Medical Research Evaluation Facility in West Jefferson, OH as described in Example 8.

EXAMPLE 11

Immunization of Mice Using Codon-Optimized *B. anthracis* DNA Vaccines

a) Experiment 1

Six groups (Groups A-F) of 5 Balb/c female mice were injected bilaterally in the rectus femoris muscle with 50 µl of DNA solution (at 1.0 mg/ml) (100 µl total/mouse), on days 1 and 21 and 42 with each of the following plasmids:

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Group 1A: VR6290 (TPA-PA63, Fig. 1, SEQ ID NO:1, prepared as described in Example 3a);

Group 1B: VR6291 (TPA-PA63 Δ FF, Fig. 2, SEQ ID NO:5, prepared as described in Example 3b);

5 Group 1C: VR6292 (TPA-PA83 Δ furin, Fig. 3, SEQ ID NO:7, prepared as described in Example 3c);

Group 1D: VR6295 (TPA-LF HEXXH, Fig. 4, SEQ ID NO:9, prepared as described in Example 4a);

Group 1E: VR6290 (50 μ g) +VR6295 (50 μ g), co-injected; and

10 Group 1F: VR1012 (empty expression vector).

The plasmids listed above were formulated as follows. One vial (0.5 mg) of MPL+TDM adjuvant, purchased from Sigma/Aldrich (catalog # M6536) was resuspended in 150 mM Na₂PO₄ according to manufacturers instructions. Fifty microliters of DNA solution was mixed 1:1 (v/v) with the MPL+TDM emulsion and injected into each mouse at the times specified above.

Mice were bled for serum on days 0 (prebleed) , 20 (bleed 1), and 41 (bleed 2), and 62 (bleed 3). PA antibodies were measured in each of Groups 1A-1C, 1E, and 1F, LF antibodies were measured in each of Groups 1D, 1E, and 1F, and LT neutralizing antibodies were measured in each of Groups 1A-1E. All assays were done as outlined in Example 9. The geometric mean of the anti-PA and anti-LF titers were calculated following each bleed. The results are shown in Figs. 15A and 15B, respectively. In Fig. 15C, the serum from each mouse was tested for LT neutralizing antibody titer after the last DNA immunization (bleed 3) according to the procedure in Example 9. The mean neutralizing titer for each group of mice was calculated and plotted and the error bars represent one standard deviation from the mean.

b) Experiment 2

30 Eight groups of 5 mice each (Groups 2A-2H) were injected bilaterally in the rectus femoris with 50 μ l (50 μ g) of DNA solution (100 μ l (100 μ g)

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total per mouse), adjuvanted with MPL + TDM as described in section 11a, on days 1, 21, and 49 with the following combinations of plasmids:

Group 2A: VR-6290 (50 µg) + VR-1012 (50 µg);

Group 2B: VR-6291 (50 µg) + VR-1012 (50 µg);

5 Group 2C: VR-6292 (50 µg) + VR-1012 (50 µg);

Group 2D: VR-6295 (50 µg) + VR-1012 (50 µg);

Group 2E: VR-6290 (50 µg) + 50 µg VR-6295

Group 2F: VR-6291 (50 µg) + VR-6295 (50 µg);

Group 2G: VR-6292 (50 µg) + VR-6295 (50 µg); and

10 Group 2H: VR-1012 (100 µg).

Mice were bled for serum on days 0 (prebleed) , 20 (bleed 1), and 41 (bleed 2), and 62 (bleed 3). PA antibodies were measured in each of Groups 2A-2C and 2E-2H, LF antibodies were measured in each of Groups 2D-2H, and LT neutralizing antibodies were measured in each of Groups 2A-2G. All assays were done as outlined in Example 9. The geometric mean of the anti-PA and anti-LF titers were calculated following each bleed. The results are shown in Figs. 16A and 16B, respectively. In Fig. 16C, the serum from each mouse was tested for LT neutralizing antibody titer after the last DNA immunization (bleed 3) according to the procedure in Example 9. The mean neutralizing titer for each group of mice was calculated and plotted and the error bars represent one standard deviation from the mean.

c) Experiment 3

Four groups of 5 mice each (Groups 3A-3D) were injected bilaterally in the rectus femoris with 50 µl (50 µg) of DNA solution (100 µl (100 µg) total per mouse), adjuvanted with MPL + TDM as described in section 11a, on days 1, 21, and 49 with the following combinations of plasmids:

Group 3A: VR-6292 (50 µg) + VR-1012 (50 µg);

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Group 3B: VR-6292 (50 µg) + VR-62952 (50 µg, TPA-LF Domain I-III, Fig. 5, SEQ ID NO:13, prepared as described in Example 4b);

Group 3C: VR-6292 (50 µg) + VR-62951 (50 µg, TPA-LF Domain IB, Fig. 14, SEQ ID NO:39, prepared as described in Example 4d); and

5 Group 3D: VR-6299 (50 µg, TPA-Sugar minus PA63, Figure 7, SEQ ID NO:17, prepared as described in Example 5a) + VR-1012 (50 µg).

Mice were bled for serum on days 0 (prebleed) , 20 (bleed 1), and 41 (bleed 2), and 62 (bleed 3). PA antibodies were measured in each of Groups 3A-3D, LF antibodies were measured in each of Groups 3B and 3C, and LT neutralizing antibodies were measured in each of Groups 3A-3D. All assays were done as outlined in Example 9. The geometric mean of the anti-PA and anti-LF titers were calculated following each bleed. The results are shown in Figs. 17A and 17B, respectively. In Fig. 17C, the serum from each mouse was tested for LT neutralizing antibody titer after the last DNA immunization (bleed 3) according to the procedure in Example 9. The mean neutralizing titer for each group of mice was calculated and plotted and the error bars represent one standard deviation from the mean.

d) Experiment 4

20 Four groups of 10 mice each (Groups 4A-4D) were injected bilaterally in the rectus femoris with 50 µl (50 µg) of of plasmid VR-6292 (100 µl (100 µg) total per mouse), formulated with various adjuvants, on days 1, 21, and 49, as follows:

Group 4A: VR-6292 formulated with CRL 1005/BAK;

25 Group 4B: VR-6292 formulated with MPL + TDM, as described in section 11a, *supra*;

Group 4C: VR-6292 formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ mass ratio; and

30 Group 4D: VR-6292 formulated with DMRIE:DOPE (1:1 molar ratio) at a 4:1 DNA:lipid mass ratio.

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The plasmids in Group 4A were formulated as follows. The poloxamer CRL1005 (from Organichem) and a solution of benzyl-alkonium chloride "BAK" (from Ruger Chemicals) were added sequentially to plasmid solutions in PBS. The initial plasmid/poloxamer formulation was prepared to contain 5 mg/mL plasmid DNA, 7.5 mg/mL CRL1005 and 0.3 mM BAK. These initial preparations were diluted 1:1 (vol:vol) with PBS, then cold sterile filtered. Further dilution with sterile PBS was done just prior to use to provide the final working concentration of 1 mg/mL pDNA, 1.5 mg/mL CRL1005 and 0.06 mM BAK.

Mice were bled for serum on days 0 (prebleed), 20 (bleed 1), and 41 (bleed 2), and 62 (bleed 3). PA antibodies were measured in each of Groups 4A-4D, and LT neutralizing antibodies were measured in each of Groups 4A-4D. All assays were done as outlined in Example 9. The geometric mean of the anti-PA titers were calculated following each bleed. The results are shown in Fig. 18A. In Fig. 18B, the serum from each mouse was tested for LT neutralizing antibody titer after the last DNA immunization (bleed 3) according to the procedure in Example 9. The mean neutralizing titer for each group of mice was calculated and plotted and the error bars represent one standard deviation from the mean.

e) Experiment 5

Six groups of 10 mice each (Groups 5A-5F) were injected bilaterally in the rectus femoris with 50 μ l (50 μ g) of of plasmid VR-6292 (100 μ l (100 μ g) total per mouse), formulated with various adjuvants, on days 1, 14, and 28, as follows:

Group 5A: VR-6292 formulated with MPL + TDM, as described in section 11a, *supra*;

Group 5B: VR-6292 formulated with MPL-A aqueous 1000 μ g/mL (Corixa) mixed 1:1 (v/v) with DNA;

Group 5C: VR-6292 formulated with CRL 1005/BAK, as described in section 11d, *supra*;

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Group 5D: VR-6292 formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ mass ratio;

Group 5E: VR-6292 formulated with DMRIE:DOPE (1:1 molar ratio) at a 4:1 DNA:lipid mass ratio; and

5 Group 5F: VR-6292 formulated with 1 X PBS.

10 Mice were bled for serum on days 0 (prebleed) , 13 (bleed 1), and 27 (bleed 2), and 56 (bleed 3). PA antibodies were measured in each of Groups 5A-5F after each bleed, and LT neutralizing antibodies were measured in each of Groups 5A-5F after bleed 3. All assays were done as outlined in Example 9. The geometric mean of the anti-PA titers were calculated following each bleed. The results are shown in Fig. 20. In Fig. 21, the serum from each mouse was tested for LT neutralizing antibody titer after the last DNA immunization (bleed 3) according to the procedure in Example 9. The mean
15 neutralizing titer for each group of mice was calculated and plotted and the error bars represent one standard deviation from the mean.

EXAMPLE 12

Immunization of Rabbits Using Codon-Optimized *B. anthracis* DNA Vaccines

20 Twelve (12) groups of 10 rabbits each (Groups A-G and I-M, for DNA vaccinations) and one group of 4 rabbits (Group H, for the AVA vaccination) (*Oryctolagus cuniculus*, New Zealand albino rabbits, 2-5 kg each at onset of treatment) were used in this experiment. The rabbits in Groups A-G and I-M received a 500 µg intramuscular injection in each quadriceps muscle (bilateral)
25 for a total of 1 mg of plasmid DNA per rabbit per immunization. Injection of the formulated plasmid DNA took place on days 0, 28, and 56. Some animals received only the first two plasmids injections on days 0 and 28 (denoted 2 injns in Fig. 19). All rabbits were prebled two days before the first immunization and bled again on days 14, 42, and 70.

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Unless noted, the various formulations were administered by a bilateral intramuscular injection into the quadriceps muscles on Days 0, 28, and 56 with a needle. The dose volume to be administered is 500 µl/muscle, 1 ml/animal. The rabbits in Group D were vaccinated using a Biojector, as follows.

5 Animals were anesthetized using ketamine/xylazine. The skin over the injection site was shaved, and the dose volume administered was 500 µl/muscle, 1 ml/animal. The vaccination groups were as follows:

Group A: VR6292 formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ ratio;

10 Group B: VR6292 (500 µg) + VR-62952 (500 µg) formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ ratio;

Group C: VR6292 formulated with DMRIE/DOPE at a 4:1 DNA:lipid ratio;

15 Group D: VR6292 formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ ratio, delivered by Biojector,

Group E: VR6292 (500 µg) + VR-62951 (500 µg) formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ ratio;

Group F: VR6290 formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ ratio;

20 Group G: VR6292 formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ ratio (two injections only);

Group H: Commercial anthrax vaccine AVA, 50 µl, delivered on day 28 and 56 by a single IM injection;

25 Group I: VR-62951 formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ ratio;

Group J: VR6292 (500 µg) + VR-62951 (500 µg) formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ ratio (two injections only);

Group K: VR-62952 formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ ratio;

30 Group L: VR6292 formulated with MPL-A aqueous 1000 µg/mL (Corixa) mixed 1:1 (v/v) with DNA;

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Group M: VR6292 formulated with CRL1005/BAK, formulated as described in Example 11d, *supra*.

5 The LT neutralization assay was performed on all rabbit sera from the day 70 bleed. The median titer \pm one standard deviation is shown for each group in Fig. 19.

EXAMPLE 13

10 Immunization and Challenge of Rabbits Using Codon-Optimized *B. anthracis* DNA Vaccines

15 Ten groups of rabbits (*Oryctolagus cuniculus*, New Zealand albino rabbits, 2-5 kg each at onset of treatment, ten (10) animals per group unless otherwise noted) were used in this experiment. These included selected groups of animals described in Example 12, as noted below. The various plasmid DNA formulations were administered by a bilateral intramuscular injection into the quadriceps muscles on Days 0, 28, and 56 with a needle. The dose volume to be administered is 500 μ l/muscle, 1 ml/animal. The vaccination groups were as follows:

20 Group 1: VR6292 formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ ratio (Group A from Example 12);

 Group 2: VR6292 formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ ratio (two injections only) (Group G from Example 12);

25 Group 3: VR6292 formulated with DMRIE/DOPE at a 4:1 DNA:lipid ratio (Group C from Example 12);

 Group 4: VR6292 (500 μ g) + VR-62951 (500 μ g) formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ ratio (two injections only) (Group J from Example 12);

30 Group 5: VR6292 (500 μ g) + VR-62952 (500 μ g) formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ ratio (Group B from Example 12);

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Group 6: VR-62952 formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ ratio (two animals) (Group K from Example 12);

Group 7: VR1012 formulated with Vaxfectin™ at a 4:1 DNA: Vaxfectin™ ratio (four animals);

5 Group 8: VR1012 formulated with DMRIE/DOPE at a 4:1 DNA:lipid ratio (two animals);

Group 9: Commercial anthrax vaccine AVA, 50 µl, delivered on 28 and 56 by a single IM injection (Group I from Example 12); and

Group 10: Twelve unvaccinated animals.

10

The rabbits in Groups 1-8 received a 500 µg intramuscular injection in each quadricep muscle (bilateral) for a total of 1 mg of plasmid DNA per rabbit per immunization. In groups 1, 3, 5, 6, 7, 8, and 9, three injections of the formulated plasmid DNA took place on days 0, 28, and 56. In groups 2 and 4, two injections of the formulated plasmid DNA took place on days 0 and 28. In group 19 commercial anthrax vaccine AVA, 50 µl, was injected intramuscularly on days 28 and 56. All rabbits were prebled two days before the first immunization and bled again on days 14, 42, and 70.

15

Over a four-day period on or around day 70 (indicated in Table 17 as "challenge days" C1-C4), the rabbits were challenged by aerosol administration of *B. anthracis* (Ames strain) spores by standard methods. See, e.g., Henderson, DW *J. Hygiene* 50:53-68 (1952)). Challenge doses ranged from about 50 LD50 equivalents to about 250 LD50 equivalents as noted in Table 17 below. The animals were monitored for morbidity and mortality at regular intervals out to days 19-22 (depending on the challenge day) following challenge. The results are shown in Table 17, and are summarized in Table 18. "NC" denotes "not challenged."

20

25

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TABLE 17

DAY			
Group 1			
1.1	C3	123.5	Y
1.2	NC		
1.3	C4	113.5	Y
1.4	C1	56.4	Y
1.5	C3	92.7	Y
1.6	C4	66.3	Y
1.7	C1	103	Y
1.8	C2	127.3	Y
1.9	NC		
1.10	C2	128.8	Y
Group 2			
2.1	C1	76	Y
2.2	C4	70.5	Y
2.3	NC		
2.4	C4	52.1	Y
2.5	C1	252.1	Y
2.6	C2	119.1	Y
2.7	C3	52.4	Y
2.8	NC		
2.9	C2	71.9	Y
2.10	C3	195.1	Y
Group 3			
3.1	C2	55.7	Y
3.2	C3	238.3	Y
3.3	C4	110	Y
3.4	C1	208.1	Y
3.5	NC		
3.6	C1	142.9	Y
3.7	C3	169	Y
3.8	NC		
3.9	C4	57.5	Y
3.10	C2	74.7	Y
Group 4			
4.1	C3	87.3	Y
4.2	C4	90.2	Y
4.3	C1	81.6	Y
4.4	NC		
4.5	C2	100	Y
4.6	C2	72	Y
4.7	C1	76.1	Y
4.8	C4	92.8	Y
4.9	NC		
4.10	C3	205	Y

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Group 5			
5.1	NC		
5.2	C1	192.2	Y
5.3	C2	152.6	Y
5.4	C4	66.6	Y
5.5	C3	135.7	Y
5.6	C2	85.1	Y
5.7	C4	79	Y
5.8	C1	126.6	Y
5.9	C3	154.7	Y
5.10	NC		
Group 6			
6.1	C4	117.7	Y
6.2	C3	241.4	N (D4)
6.3	NC		
6.4	C1	107.3	Y
6.5	C4	58.7	N (D4)
6.6	C3	121	Y
6.7	C3	160.8	Y
6.8	C2	46.1	N (D7)
6.9	C1	195.2	N (D6)
6.10	C2	94.5	Y
Group 7			
7.1	C3	101.9	N (D3)
7.2	C4	144.1	N (D2)
7.3	NC		
7.4	C1	108.2	N (D2)
Group 8			
8.1	C2	63	N (D3)
8.2	C4	58.2	N (D3)
Group 9			
9.1	C2	113.4	Y
9.2	C1	106.9	Y
9.3	C3	157.6	Y
9.4	C4	175.6	Y
Group 10			
10.1	C4	76.7	N (D2)
10.2	C3	207.6	N (D3)
10.3	C2	91.5	N (D2)
10.4	C4	176	N (D2)
10.5	C2	123	N (D3)
10.6	C2	95.4	N (D3)
10.7	C4	91.5	N (D3)
10.8	C1	165.2	N (D2)
10.9	C1	57.3	N (D3)
10.10	C3	163.8	N (D4)
10.11	C3	114.2	N (D2)
10.12	C1	62.3	N (D2)

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TABLE 18

Group	Survival
1	8/8 (100%)
2	8/8 (100%)
3	8/8 (100%)
4	8/8 (100%)
5	8/8 (100%)
6	5/9 (56%)
7	0/2 (0%)
8	0/3
9	4/4 (100%)
10	0/12 (0%)

5

EXAMPLE 14

Immunization of Mice using Single Vial Formulations

Single vial formulations were prepared by reconstituting bulk DMRIE and DOPE lipids to form multi-lamellar vesicles (MLV). These vesicles were then further processed to produce small DMRIE and DOPE liposomes (SUV) and sterile filtered through a 0.2 μ m membrane. The formulations were prepared aseptically at room temperature by adding sterile plasmid DNA and sterile DMRIE:DOPE SUV liposomes into separate feed lines and then combining into a third sterile vessel via in-line mixing. Moderate rates of addition and moderate in-vessel mixing were used to form a lipid/plasmid DNA complex. Preparation of lipids and lipid/plasmid DNA complexes is described in Zelphati *et al. Gene Therapy* 5: 1277-1282 (1998) which is incorporated herein by reference in its entirety. The formulations described below contain final molar ratios of 4:1 or 2:1 plasmid DNA to DMRIE.

Eight groups of mice, containing 10 mice in each group, were injected bilaterally in the rectus femoris muscle with the various formulations described below. Each injection contained 50 μ g of purified plasmid VR6292 (PA83 Δ furin) in a volume of 0.1ml. At 0, 2 and 4 weeks the groups were injected with the following formulations, all containing 50 μ g of VR6292

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plasmid DNA (prepared as described in the plasmid DNA purification section prior to Example 1).

5 Group A: Unextruded MLV, in a 4:1 molar ratio of plasmid DNA to DMRIE, in PBS (pH 7.2). The formulation was freshly prepared just prior to injection.

10 Group B: Unextruded MLV, in a 4:1 molar ratio of plasmid DNA to DMRIE, in 10% sucrose and 10mM sodium phosphate, pH 7.2. The formulation was freshly prepared just prior to injection.

15 Group C: 0.2 μ m filter extruded (SUV) liposomes, in a 4:1 molar ratio of plasmid DNA to DMRIE, in 10% sucrose and 10mM sodium phosphate (pH 7.2). The formulation was stored overnight at 2-8°C prior to inoculation.

20 Group D: SUV liposomes, in a 4:1 ratio plasmid DNA to DMRIE, in 10% sucrose and 10mM sodium phosphate, pH 7.2. The formulation was frozen prior to inoculation.

 Group E: SUV liposomes, in a 4:1 molar ratio of plasmid DNA to DMRIE, in 10% sucrose and 10mM sodium phosphate, pH 7.2. The formulation was lyophilized prior to inoculation.

25 Group F: Unextruded MLV, containing cholesterol in place of DOPE, in a 4:1 molar ratio of plasmid DNA to DMRIE, in 10% sucrose and 10mM sodium phosphate, pH 7.2. The formulation was freshly prepared just prior to injection.

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Group G: Unextruded MLV, in a 2:1 molar ratio of plasmid DNA to DMRIE, in PBS, pH 7.2. The formulation was freshly prepared just prior to injection.

5 Group H: SUV liposomes, in a 2:1 molar ratio of plasmid DNA to DMRIE, in 10% sucrose and 10mM sodium phosphate, pH 7.2. The formulation was stored overnight at 2-8°C prior to injection.

10 Mice were bled for serum prior to each DNA immunization at week 0 (Prebleed), week 2 (Bleed 1), week 4 (Bleed 2) and four weeks post the last injection (Bleed 3). Anti-PA IgG antibody titers and neutralization of lethal toxin (Letx) titers were performed as described in Example 9. The antibody titers and neutralization results for each bleed and every formulation tested are shown in Tables 19 and 20.

15

TABLE 19: Anti - PA IgG Titer

Group		A	B	C	D
Geometric Mean	Prebleed	80	80	80	80
	Bleed 1	10975	4165	7760	4457
	Bleed 2	305736	66540	108094	62084
	Bleed 3	1616014	376405	376405	655627
Std. Dev.	Prebleed	0	0	0	0
	Bleed 1	11372	7630	23983	12421
	Bleed 2	215705	58765	84998	51642
	Bleed 3	639310	370406	343674	1200361

Group		E	F	G	H
Geometric Mean	Prebleed	80	80	80	80
	Bleed 1	7760	5487	9554	4457
	Bleed 2	81920	71316	327680	76434
	Bleed 3	1310720	266159	1310987	351199
Std. Dev.	Prebleed	0	0	0	0
	Bleed 1	15017	8172	23498	26219
	Bleed 2	116014	55555	205073	53970
	Bleed 3	0	197337	678738	221840

20

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TABLE 20: Letx Neutralizing Antibody Titers

Group	A	B	C	D
Mean	184	226	160	149
Std. Dev.	217	372	178	390

Group	E	F	G	H
Mean	92	86	211	35
Std. Dev.	111	89	212	46

EXAMPLE 15

Immunization of Non-Human Primates Using Codon-Optimized *B. anthracis*
DNA Vaccines

Three groups of cynomologous macaques (*M. fascicularis*), containing three monkeys in each group, were used in this experiment. The animals were immunized unilaterally, intramuscularly, in the deltoid muscle with a Bioinjector device. Varying amounts of purified VR6292 (PA83Δfurin) plasmid DNA (prepared as described in the plasmid DNA purification section prior to Example 1) formulated with Vaxfectin™, in a 4:1 molar ratio of plasmid DNA to lipid, was used in all inoculations in this study. All animals received injections at month 0, 1 month, and 2 months. Group 1 received 20μg of plasmid DNA at each inoculation. Group 2 received 100μg of plasmid DNA at each inoculation. Group 3 received 200μg of plasmid DNA at each inoculation.

The monkeys were bled for serum prior to each DNA immunization at month 0 (Bleed 1), month 1 (Bleed 2), month 2 (Bleed 3) and at four weeks after the last injection (Bleed 4). Anti-PA IgG antibody titers and neutralization of lethal toxin (Letx) titers were performed as described in Example 9. The antibody titers and neutralization results for each group of animals are shown in Tables 21, 22 and 23.

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2 out of 3 animals in Group 1 generated an anti-PA IgG titer. One of the animals generated a sizable titer (20,000) after three injections. This titer is comparable to the titers of the animals in groups receiving higher doses of plasmid DNA (Groups 2 and 3). None of the animals in Group 1 generated any measurable neutralization activity of Letx at the lowest dilutions tested (serum diluted 1:20).

The animals in Groups 2 and 3 generated similar immune responses to the inoculations. All monkeys in both groups developed anti-PA IgG titers. Letx neutralization titers were generated in 2 out of 3 monkeys in both groups. The remaining animal in each group had measurable neutralization activity, but below the level needed to score a titer.

TABLE 21: Group 1 – Anti-PA IgG and LetX Neutralizing Titers

Animal #		1001	1002	1003
	Bleed 2	80	160	640
	Bleed 3	80	640	10240
	Bleed 4		2560	20480
	Letx Neutralizing Titer			
	Bleed 3	0	0	0
	Bleed 4	0	0	0

TABLE 22: Group 2 - Anti-PA IgG and LetX Neutralizing Titers

Animal #	Anti-PA IgG	2001	2002	2003
	Bleed 2	640	10240	5120
	Bleed 3	10240	20480	40960
	Bleed 4	40960	40960	81920
	Letx Neutralization Titer			
	Bleed 3	0	***	***
	Bleed 4	***	40	80

*** denotes a detectable low level of neutralization activity

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TABLE 23: Group 3 - Anti-PA IgG and LetX Neutralizing Titers

Anti-PA IgG				
Animal #		3001	3002	3003
	Bleed 2	640	320	640
	Bleed 3	5120	20480	10240
	Bleed 4	20480	20480	81920
LetX Neutralizing Titer				
	Bleed 3	0	40	***
	Bleed 4	***	160	80

*** denotes a detectable low level of neutralization activity

5

EXAMPLE 16

Immunization Challenge of Rabbits Using Codon-Optimized *B. anthracis* DNA
Vaccines

10 a) Long-Term Immune Response in DNA Immunized Rabbits

10 rabbits immunized, as described in Example 12, Group D (Immunized three times with VR6292), were followed long-term for anti-PA antibody titer, LetX neutralization titer and protective immune response to an anthrax spore challenge. Anti-PA IgG antibody titers and LetX neutralization titers were performed as described in Example 9. The results of the titers and neutralization assays are shown in Table 24. Rabbits were bled twelve times on the weeks indicated in Table 24.

On week 39 of the experiment, rabbits were challenged by aerosol administration of *B. anthracis* (Ames strain) spores by standard methods as described in Example 13. All rabbits survived. Control animals that were not vaccinated did not survive challenge.

25

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TABLE 24

<i>Anti-P8 IgG Serum Antibody Titer</i>		
Week (post first injection)	Geometric Mean	Std. Dev.
2	20480	22744
6	2622775	1635799
10	12909485	6079129
14	6456057	8244196
18	4565122	7496131
22	2810448	2931335
26	1311120	1508050
30	1311120	1508050
34	1405367	888676
39	1064744	1475391
40	1505928	1809833
42	2129704	1865167
<i>Letx Neutralization Titer</i>		
Week (post first injection)	Geometric Mean	Std. Dev.
6	1576	843
10	4457	2956
14	2560	1602
18	1372	1441
22	1194	1455
26	970	607
30	905	641
35	905	641
40	844	843
41	1040	911
43	1194	955

5 b) Rabbit Immunization Dosing with Intended Human Vaccine Product

10 Sixty New Zealand White rabbits (30 males and 30 females), approximately 10-12 weeks old, were used for this study. Ten animals per sex were injected with the formulations described below. The plasmids were formulated with DMRIE/DOPE in a 4:1 DNA to lipid mass ratio in PBS, as described in Example 8b.

Group 1: 1.0ml of PBS

Group 2: 0.1mg of plasmid VR-6292 and 0.1mg of

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plasmid VR 62952.

Group 3: 1.0mg of plasmids VR-6292 and 1.0mg VR-62952.

5 All animals in the study received unilateral intramuscular injections into the vastus lateralis muscle at 0, 2, 4 and 8 weeks.

Serum samples were taken from all study animals once during the pre-treatment period and once during weeks 2, 4, 6, 8, 10 and 12. Anti-PA and LF antibody titers and Letx neutralizing antibody titers were evaluated using serum samples taken prior to immunization and at 8 weeks prior to the fourth DNA immunization. All immunological assays were performed as described in Example 9. Anti-PF and LF antibody titers and Letx neutralizing antibody results for the bleeds taken at week 8 are shown in Tables 25 and 26.

15 TABLE 25: Anti-PA and Anti-LF Antibody Titers (Geometric Mean)

Group	2	3
Anti-PA	163840	514211
Anti-LF	163840	678540
Std. Dev.		
Anti-PA	230686	595754
Anti-LF	386254	730464

TABLE 26: Letx Neutralization Titers (Geometric Mean)

20

Group	2	3
Letx titer	889	2840
Std Dev	510	1518

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c) Post Challenge Immune Responses in Aerosolized Spore Challenged Rabbits.

Six groups of rabbits, with 10 individuals in each group, were immunized as described for Groups A-C, G, H and K in Example 12. 39 weeks after the last immunization, these rabbits were challenged with anthrax aerosolized spores, as described in Example 13. Control animals that had not been immunized were also challenged as described in Example 13. No control animal survived the challenge.

At one day prior to challenge, and at 7 and 21 days post challenge, animals were bled for serum. Anti-PA and LF IgG antibody and LetX neutralizing titers were performed as described in Example 9. It should be noted that except as described below, immunized animals had developed protective immunity since they survived challenge.

The immune responses post challenge could be divided into two groups: rabbits that showed no increase in immune response after challenge (lack of boosting) and rabbits that were boosted in their response to PA and/or LF after spore challenge.

All rabbits immunized as described for Groups A-C, in Example 12 (immunized with VR6292 or VR6292+VR62952, three times), demonstrated a lack of boosting. Two rabbits immunized as described for Group G, in Example 12 (immunized with VR6292 twice), had the lowest anti-PA titers pre-challenge and demonstrated a small post-challenge boost in anti-PA titer and the generation of an anti-LF response.

Several rabbits immunized as described for Group K, in Example 12 (immunized with VR62952 (LF[I-III])), did not survive anthrax spore challenge. The five surviving rabbits all had significant anti-PA titers post challenge. Additionally rabbits immunized as described for Group H in Example 12 (immunized twice with the commercial anthrax vaccine AVA), had no measurable anti-LF response pre-challenge. After challenge all rabbits

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showed a boosted anti-PA titer and the generation of a strong anti-LF response.

In summary, all rabbits immunized two or three times with plasmids encoding PA or PA+LF generated strong immune responses and were able to survive anthrax spore challenge. Almost all of these rabbits showed a lack of immune response boosting post-challenge, which is consistent with sterilizing immunity. In contrast, rabbits immunized twice with 50 μ l of AVA exhibited a strong anti-LF response and a boosted anti-PA titer.

EXAMPLE 17

Mucosal Vaccination and Electrically Assisted Plasmid Delivery

a) Mucosal DNA Vaccination

Plasmid constructs comprising codon-optimized and non-codon-optimized coding regions encoding LF, PA or various fragments, variants or derivatives, as described herein, are delivered to BALB/c mice at 0, 2 and 4 weeks via i.m., intranasal (i.n.), intravenous (i.v.), intravaginal (i.vag.), intrarectal (i.r.) or oral routes. The DNA is delivered unformulated or formulated with the cationic lipids DMRIE/DOPE (DD), DMRIE/Cholesterol or Vaxfectin™. Serum IgG titers against the various LF and PA antigens are measured as described in Example 9, as well as Letx neutralization titers.

b) Electrically-assisted plasmid delivery

In vivo gene delivery may be enhanced through the application of brief electrical pulses to injected tissues, a procedure referred to herein as electrically-assisted plasmid delivery. See, e.g., Aihara, H. & Miyazaki, J. *Nat. Biotechnol.* 16:867-70 (1998); Mir, L.M. *et al.*, *Proc. Natl Acad. Sci. USA* 96:4262-67 (1999); Hartikka, J. *et al.*, *Mol. Ther.* 4:407-15 (2001); and Mir, L.M. *et al.*; Rizzuto, G. *et al.*, *Hum Gene Ther* 11:1891-900 (2000);

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Widera, G. *et al*, *J. of Immuno.* 164: 4635-4640 (2000). The use of electrical pulses for cell electroporation has been used to introduce foreign DNA into prokaryotic and eukaryotic cells *in vitro*. Cell permeabilization can also be achieved locally, *in vivo*, using electrodes and optimal electrical parameters that are compatible with cell survival.

The electroporation procedure can be performed with various electroporation devices. These devices include external plate type electrodes or invasive needle/rod electrodes and can possess two electrodes or multiple electrodes placed in an array. Distances between the plate or needle electrodes can vary depending upon the number of electrodes, size of target area and treatment subject.

The TriGrid needle array, used in examples described herein, is a three electrode array comprising three elongate electrodes in the approximate shape of a geometric triangle. Needle arrays may include single, double, three, four, five, six or more needles arranged in various array formations. The electrodes are connected through conductive cables to a high voltage switching device that is connected to a power supply.

The electrode array is placed into the muscle tissue, around the site of nucleic acid injection, to a depth of approximately 3 mm to 3 cm. The depth of insertion varies depending upon the target tissue and size of patient receiving electroporation. After injection of foreign nucleic acid, such as plasmid DNA, and a period of time sufficient for distribution of the nucleic acid, square wave electrical pulses are applied to the tissue. The amplitude of each pulse ranges from about 100 volts to about 1500 volts, *e.g.*, about 100 volts, about 200 volts, about 300 volts, about 400 volts, about 500 volts, about 600 volts, about 700 volts, about 800 volts, about 900 volts, about 1000 volts, about 1100 volts, about 1200 volts, about 1300 volts, about 1400 volts, or about 1500 volts or about 1-1.5kV/cm, based on the spacing between electrodes. Each pulse has a duration of about 1 μ s to about 1000 μ s, *e.g.*, about 1 μ s, about 10 μ s, about 50 μ s, about 100 μ s, about 200 μ s, about 300 μ s, about 400 μ s, about 500 μ s, about 600 μ s, about 700 μ s, about 800 μ s, about

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900 μ s, or about 1000 μ s, and a pulse frequency on the order of about 1-10 Hz. The polarity of the pulses may be reversed during the electroporation procedure by switching the connectors to the pulse generator. Pulses are repeated multiple times. The electroporation parameters (*e.g.* voltage
5 amplitude, duration of pulse, number of pulses, depth of electrode insertion and frequency) will vary based on target tissue type, number of electrodes used and distance of electrode spacing, as would be understood by one of ordinary skill in the art.

Immediately after completion of the pulse regimen, subjects receiving
10 electroporation can be optionally treated with membrane stabilizing agents to prolong cell membrane permeability as a result of the electroporation. Examples of membrane stabilizing agents include, but are not limited to, steroids (*e.g.* dexamethasone, methylprednisone and progesterone), angiotensin II and vitamin E. A single dose of dexamethasone, approximately
15 0.1 mg per kilogram of body weight, should be sufficient to achieve a beneficial affect.

EAPD techniques such as electroporation can also be used for plasmids contained in liposome formulations. The liposome -- plasmid suspension is administered to the animal or patient and the site of injection is treated with a
20 safe but effective electrical field generated, for example, by a TriGrid needle array. The electroporation may aid in plasmid delivery to the cell by destabilizing the liposome bilayer so that membrane fusion between the liposome and the target cellular structure occurs. Electroporation may also aid in plasmid delivery to the cell by triggering the release of the plasmid, in high
25 concentrations, from the liposome at the surface of the target cell so that the plasmid is driven across the cell membrane by a concentration gradient via the pores created in the cell membrane as a result of the electroporation.

Female BALB/c mice aged 8-10 weeks are anesthetized with inhalant isoflurane and maintained under anesthesia for the duration of the
30 electroporation procedure. The legs are shaved prior to treatment. Plasmid constructs comprising codon-optimized and non-codon-optimized coding

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regions which encode LF, PA or various fragments, variants or derivatives, as described herein, are administered to BALB/c mice ($n = 10$) via unilateral injection in the quadriceps, with 50 μ g total of a plasmid DNA per mouse, using an 0.3 cc insulin syringe and a 26 gauge, 1/2 length needle fitted with a plastic collar to regulate injection depth. Approximately one minute after injection, electrodes are applied. Modified caliper electrodes are used to apply the electrical pulse. See Hartikka J. *et al. Mol Ther* 188:407-415 (2001). The caliper electrode plates are coated with conductivity gel and applied to the sides of the injected muscle before closing to a gap of 3 mm for administration of pulses. EAPD is applied using a square pulse type at 1-10 Hz with a field strength of 100-500 V/cm, 1-10 pulses, of 10-100 ms each.

Mice are vaccinated \pm EAPD at 0, 2 and 4 weeks. As endpoints, serum IgG titers against the various LF and PA antigens are measured as described in Example 9, as well as Letx neutralization titers.

Rabbits ($n = 3$) are given bilateral injections in the quadriceps muscle with plasmid constructs comprising codon-optimized and non-codon-optimized coding regions which encode LF, PA or various fragments, variants or derivatives, as described herein. The implantation area is shaved and the TriGrid electrode array is implanted into the target region of the muscle. 3.0 mg of plasmid DNA is administered per dose through the injection port of the electrode array. An injection collet is used to control the depth of injection. Electroporation begins approximately one minute after injection of the plasmid DNA is complete. Electroporation is administered with a TriGrid needle array, with electrodes evenly spaced 7mm apart, using an Ichor TGP-2 pulse generator. The array is inserted into the target muscle to a depth of about 1 to 2 cm. 4-8 pulses are administered. Each pulse has a duration of about 50-100 μ s, an amplitude of about 1-1.2kV/cm and a pulse frequency of 1 Hz. The injection and electroporation may be repeated.

Sera are collected from vaccinated rabbits at various time point. As endpoints, serum IgG titers against the various LF and PA antigens are measured as described in Example 9, as well as Letx neutralization titers.

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To test the effect of electroporation on therapeutic protein expression in non-human primates, male or female cynomolgous macaques are given either 2 or 6 i.m. injections of plasmid constructs comprising codon-optimized and non-codon-optimized coding regions which encode LF, PA or various fragments, variants or derivatives, as described herein, (0.1 to 10 mg DNA total per animal). Target muscle groups include, but are not limited to, bilateral rectus femoris, cranial tibialis, biceps, gastrocnemius or deltoid muscles. The target area is shaved and a needle array, comprising between 4 and 10 electrodes, spaced between 0.5-1.5 cm apart, is implanted into the target muscle. Once injections are complete, a sequence of brief electrical pulses are applied to the electrodes implanted in the target muscle using an Ichor TGP-2 pulse generator. The pulses have an amplitude of approximately 120 – 200V. The pulse sequence is completed within one second. During this time, the target muscle may make brief contractions or twitches. The injection and electroporation may be repeated.

Sera are collected from vaccinated monkeys at various time points. As endpoints, serum IgG titers against the various LF and PA antigens are measured as described in Example 9, as well as Letx neutralization titers.

The present invention is not to be limited in scope by the specific embodiments described which are intended as single illustrations of individual aspects of the invention, and any compositions or methods which are functionally equivalent are within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

All publications and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual

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publication or patent application was specifically and individually indicated to be incorporated by reference.

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WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 50 contiguous amino acids of SEQ ID NO:4, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region
5 for the polypeptide of SEQ ID NO:4;
wherein about 11 of the 24 phenylalanine codons in said coding region are TTT and about 13 of said phenylalanine codons are TTC;
wherein about 5 of the 62 leucine codons in said coding region are TTA, about 8 of said leucine codons are TTG, about 8 of said leucine
10 are CTT, about 12 of said leucine codons are CTC, about 4 of said leucine codons are CTA, and about 25 of said leucine codons are CTG;
wherein about 20 of the 57 isoleucine codons in said coding region are ATT, about 28 of said isoleucine codons are ATC, and about 9 of said
isoleucine codons are ATA;
15 wherein the 10 methionine codons in said coding region are ATG;
wherein about 8 of the 43 valine codons in said coding region are GTT, about 10 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 20 of said valine codons are GTG;
wherein about 13 of the 72 serine codons in said coding region are
20 TCT, about 16 of said serine codons are TCC, about 11 of said serine codons are TCA, about 4 of said serine codons are TCG, about 11 of said serine codons are AGT, and about 17 of said serine codons are AGC;

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wherein about 8 of the 29 proline codons in said coding region are CCT, about 10 of said proline codons are CCC, about 8 of said proline codons are CCA, and about 3 of said proline codons are CCG;

5 wherein about 14 of the 58 threonine codons in said coding region are ACT, about 21 of said threonine codons are ACC, about 16 of said threonine codons are ACA, and about 7 of said threonine codons are ACG;

wherein about 11 of the 41 alanine codons in said coding region are GGT, about 17 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

10 wherein about 12 of the 28 tyrosine codons in said coding region are TAT and about 16 of said tyrosine codons are TAC;

wherein about 4 of the 10 histidine codons in said coding region are CAT and about 6 of said histidine codons are CAC;

15 wherein about 8 of the 31 glutamine codons in said coding region are CAA and about 23 of said glutamine codons are CAG;

wherein about 32 of the 69 asparagine codons in said coding region are AAT and about 37 of said asparagine codons are AAC;

wherein about 25 of the 60 lysine codons in said coding region are AAA and about 35 of said lysine codons are AAG;

20 wherein about 22 of the 47 aspartic acid codons in said coding region are GAT and about 25 of said aspartic acid codons are GAC;

wherein about 21 of the 51 glutamic acid codons in said coding region are GAA and about 30 of said glutamic acid codons are GAG;

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wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 2 of the 29 arginine codons in said coding region are CGT, about 6 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 6 of said arginine codons are AGG; and

wherein about 6 of the 36 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 9 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

10 2. The polynucleotide of claim 1, wherein said nucleic acid fragment encodes at least 100 contiguous amino acids of SEQ ID NO:4.

3. The polynucleotide of claim 2, wherein said nucleic acid fragment encodes amino acids 199 to 764 of SEQ ID NO:4.

15

4. The polynucleotide of claim 3, wherein said nucleic acid fragment comprises nucleotides 82 to 1782 of SEQ ID NO:1.

5. The polynucleotide of any one of claims 1-4, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

20

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6. The polynucleotide of claim 5, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

5 7. The polynucleotide of claim 6, wherein said heterologous polypeptide is a secretory signal peptide.

8. The polynucleotide of claim 7, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

10

9. The polynucleotide of claim 8, comprising nucleotides 13-1782 of SEQ ID NO:1.

10. The polynucleotide of claim 9, comprising SEQ ID NO:1.

15

11. The polynucleotide of claim 1, wherein said nucleic acid fragment encodes amino acids 30 to 764 of SEQ ID NO:4.

12. The polynucleotide of claim 11, wherein said nucleic acid
20 fragment is ligated to a heterologous nucleic acid.

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13. The polynucleotide of claim 12, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

5 14. The polynucleotide of claim 13, wherein said heterologous polypeptide is a secretory signal peptide.

15. The polynucleotide of claim 14, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

10

16. The polynucleotide of claim 11, wherein said nucleic acid fragment comprises nucleotides 88 to 2292 of SEQ ID NO:23.

17. The polynucleotide of any one of claims 1-16, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

15

18. The polynucleotide of any one of claims 1-16, which is RNA.

19. The polynucleotide of claim 18, which is messenger RNA (mRNA).

20

20. A vector comprising the polynucleotide of any one of claims 1-17.

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21. The vector of claim 20, which is a plasmid.

22. A composition comprising the polynucleotide of any one of
5 claims 1-19, and a carrier.

23. The composition of claim 21, further comprising a component
selected from the group consisting of an adjuvant, and a transfection
facilitating compound.

10

24. The composition of claim 23, wherein said adjuvant is selected
from the group consisting of:

(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-
1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

15

a cytokine;

mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL +
TDM);

a solubilized mono-phosphoryl lipid A formulation; and

CRL1005/BAK.

20

25. The composition of claim 24, wherein said adjuvant
comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-

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tetradecenyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE),

1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and

5 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

26. The composition of claim 25, wherein said neutral lipid is DPyPE.

10 27. The composition of claim 23, comprising the transfection facilitating compound (\pm)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide (DMRJE).

15 28. A method to treat or prevent anthrax infection in a vertebrate comprising: administering to a vertebrate in need thereof the composition of any one of claims 22-27.

20 29. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to amino acids 199 to 764 of SEQ ID NO:4, wherein said nucleic acid fragment is a variant fragment of an optimized coding region for the polypeptide of SEQ ID NO:4; wherein about 11 of the 24 phenylalanine codons in said coding region are TTT and about 13 of said phenylalanine codons are TTC;

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wherein about 5 of the 62 leucine codons in said coding region are TTA, about 8 of said leucine codons are TTG, about 8 of said leucine codons are CTT, about 12 of said leucine codons are CTC, about 4 of said leucine codons are CTA, and about 25 of said leucine codons are CTG;

5 wherein about 20 of the 57 isoleucine codons in said coding region are ATT, about 28 of said isoleucine codons are ATC, and about 9 of said isoleucine codons are ATA;

 wherein the 10 methionine codons in said coding region are ATG;

 wherein about 8 of the 43 valine codons in said coding region are GTT,
10 about 10 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 20 of said valine codons are GTG;

 wherein about 13 of the 72 serine codons in said coding region are TCT, about 16 of said serine codons are TCC, about 11 of said serine codons are TCA, about 4 of said serine codons are TCG, about 11 of said serine
15 codons are AGT, and about 17 of said serine codons are AGC;

 wherein about 8 of the 29 proline codons in said coding region are CCT, about 10 of said proline codons are CCC, about 8 of said proline codons are CCA, and about 3 of said proline codons are CCG;

 wherein about 14 of the 58 threonine codons in said coding region are
20 ACT, about 21 of said threonine codons are ACC, about 16 of said threonine codons are ACA, and about 7 of said threonine codons are ACG;

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wherein about 11 of the 41 alanine codons in said coding region are GGT, about 17 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

5 wherein about 12 of the 28 tyrosine codons in said coding region are TAT and about 16 of said tyrosine codons are TAC;

wherein about 4 of the 10 histidine codons in said coding region are CAT and about 6 of said histidine codons are CAC;

wherein about 8 of the 31 glutamine codons in said coding region are CAA and about 23 of said glutamine codons are CAG;

10 wherein about 32 of the 69 asparagine codons in said coding region are AAT and about 37 of said asparagine codons are AAC;

wherein about 25 of the 60 lysine codons in said coding region are AAA and about 35 of said lysine codons are AAG;

15 wherein about 22 of the 47 aspartic acid codons in said coding region are GAT and about 25 of said aspartic acid codons are GAC;

wherein about 21 of the 51 glutamic acid codons in said coding region are GAA and about 30 of said glutamic acid codons are GAG;

wherein the 7 tryptophan codons in said coding region are TGG;

20 wherein about 2 of the 29 arginine codons in said coding region are CGT, about 6 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 6 of said arginine codons are AGG; and

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wherein about 6 of the 36 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 9 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

5 30. The polynucleotide of claim 29, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to amino acids 199 to 764 of SEQ ID NO:4.

10 31. The polynucleotide of claim 29, wherein the codons in said nucleic acid fragment corresponding to amino acids 342 and 343 of SEQ ID NO:4 are deleted.

15 32. The polynucleotide of claim 31, wherein said nucleic acid fragment encodes amino acids 24 to 587 of SEQ ID NO:6.

 33. The polynucleotide of claim 32, which comprises nucleotides 82 to 1773 of SEQ ID NO:5.

20 34. The polynucleotide of claim 29, wherein the asparagine codons in said nucleic acid fragment corresponding to amino acids 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 are deleted and each of said asparagine codons is replaced with a codon which codes for an amino acid other than asparagine.

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35. The polynucleotide of claim 34, wherein the asparagine codons in said nucleic acid fragment corresponding to amino acids 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 are deleted and each of said asparagine codons replaced with a codon which codes for glutamine.

36. The polynucleotide of claim 35, wherein said nucleic acid fragment encodes amino acids 24 to 589 of SEQ ID NO:18.

37. The polynucleotide of claim 36, which comprises nucleotides 82 to 1779 of SEQ ID NO:17.

38. The polynucleotide of claim 31, wherein the asparagine codons in said nucleic acid fragment corresponding to amino acids 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 are deleted and each of said asparagine codons is replaced with a codon which codes for an amino acid other than asparagine.

39. The polynucleotide of claim 38, wherein the asparagine codons in said nucleic acid fragment corresponding to amino acids 39, 153, 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 are deleted and each of said asparagine codons replaced with a codon which codes for glutamine.

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40. The polynucleotide of any one of claims 29-39, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

5 41. The polynucleotide of claim 40, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

10 42. The polynucleotide of claim 41, wherein said heterologous polypeptide is a secretory signal peptide.

43. The polynucleotide of claim 42, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

15 44. The polynucleotide of any one of claims 29-43, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

45. The polynucleotide of any one of claims 29-43, which is RNA.

20 46. The polynucleotide of claim 45, which is messenger RNA (mRNA).

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47. A vector comprising the polynucleotide of any one of claims
29-44.

48. The vector of claim 47, which is a plasmid.

5

49. A composition comprising the polynucleotide of any one of
claims 29-46, and a carrier.

50. The composition of claim 49, further comprising a component
10 selected from the group consisting of an adjuvant, and a transfection
facilitating compound.

51. The composition of claim 50, wherein said adjuvant is selected
from the group consisting of:

15 (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradecenyl-oxy)-
1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;
a cytokine;
mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL +
TDM);
20 a solubilized mono-phosphoryl lipid A formulation; and
CRL1005/BAK.

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52. The composition of claim 51, wherein said adjuvant comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

- 5 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE),
 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and
 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

53. The composition of claim 52, wherein said neutral lipid is
10 DPyPE.

54. The composition of claim 50, comprising the transfection facilitating compound (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

15

55. A method to treat or prevent anthrax infection in a vertebrate comprising: administering to a vertebrate in need thereof the composition of any one of claims 49-54.

20 56. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to amino acids 30 to 764 of SEQ ID NO:4, wherein said nucleic acid fragment is a variant fragment of an optimized coding region for the polypeptide of SEQ ID NO:4;

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wherein about 11 of the 24 phenylalanine codons in said coding region are TTT and about 13 of said phenylalanine codons are TTC;

5 wherein about 5 of the 62 leucine codons in said coding region are TTA, about 8 of said leucine codons are TTG, about 8 of said leucine codons are CTT, about 12 of said leucine codons are CTC, about 4 of said leucine codons are CTA, and about 25 of said leucine codons are CTG;

wherein about 20 of the 57 isoleucine codons in said coding region are ATT, about 28 of said isoleucine codons are ATC, and about 9 of said isoleucine codons are ATA;

10 wherein the 10 methionine codons in said coding region are ATG;

wherein about 8 of the 43 valine codons in said coding region are GTT, about 10 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 20 of said valine codons are GTG;

15 wherein about 13 of the 72 serine codons in said coding region are TCT, about 16 of said serine codons are TCC, about 11 of said serine codons are TCA, about 4 of said serine codons are TCG, about 11 of said serine codons are AGT, and about 17 of said serine codons are AGC;

20 wherein about 8 of the 29 proline codons in said coding region are CCT, about 10 of said proline codons are CCC, about 8 of said proline codons are CCA, and about 3 of said proline codons are CCG;

wherein about 14 of the 58 threonine codons in said coding region are ACT, about 21 of said threonine codons are ACC, about 16 of said threonine codons are ACA, and about 7 of said threonine codons are ACG;

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wherein about 11 of the 41 alanine codons in said coding region are GGT, about 17 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 12 of the 28 tyrosine codons in said coding region are
5 TAT and about 16 of said tyrosine codons are TAC;

wherein about 4 of the 10 histidine codons in said coding region are CAT and about 6 of said histidine codons are CAC;

wherein about 8 of the 31 glutamine codons in said coding region are CAA and about 23 of said glutamine codons are CAG;

10 wherein about 32 of the 69 asparagine codons in said coding region are AAT and about 37 of said asparagine codons are AAC;

wherein about 25 of the 60 lysine codons in said coding region are AAA and about 35 of said lysine codons are AAG;

15 wherein about 22 of the 47 aspartic acid codons in said coding region are GAT and about 25 of said aspartic acid codons are GAC;

wherein about 21 of the 51 glutamic acid codons in said coding region are GAA and about 30 of said glutamic acid codons are GAG;

wherein the 7 tryptophan codons in said coding region are TGG;

20 wherein about 2 of the 29 arginine codons in said coding region are CGT, about 6 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 6 of said arginine codons are AGG; and

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wherein about 6 of the 36 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 9 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

5 57. The polynucleotide of claim 56, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to amino acids 30 to 764 of SEQ ID NO:4.

10 58. The polynucleotide of claim 56, wherein the codons in said nucleic acid fragment corresponding to amino acids 192 to 197 of SEQ ID NO:4 are deleted.

15 59. The polynucleotide of claim 58, wherein said nucleic acid fragment encodes amino acids 24 to 752 of SEQ ID NO:8.

 60. The polynucleotide of claim 59, which comprises nucleotides 82 to 2268 of SEQ ID NO:7.

20 61. The polynucleotide of claim 56, wherein the asparagine codons in said nucleic acid fragment corresponding to amino acids 39, 153, 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 are deleted and each of said asparagine codons is replaced with a codon which codes for an amino acid other than asparagine.

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62. The polynucleotide of claim 61, wherein the asparagine codons
in said nucleic acid fragment corresponding to amino acids 39, 153, 275, 321,
357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 are deleted and
each of said asparagine codons replaced with a codon which codes for
5 glutamine.

63. The polynucleotide of claim 58, wherein the asparagine codons
in said nucleic acid fragment corresponding to amino acids 39, 153, 275, 321,
357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 are deleted and
10 each of said asparagine codons is replaced with a codon which codes for an
amino acid other than asparagine.

64. The polynucleotide of claim 63, wherein the asparagine codons
in said nucleic acid fragment corresponding to amino acids 39, 153, 275, 321,
15 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:AP are deleted and
each of said asparagine codons replaced with a codon which codes for
glutamine.

65. The polynucleotide of any one of claims 56-64, wherein said
20 nucleic acid fragment is ligated to a heterologous nucleic acid.

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66. The polynucleotide of claim 65, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

5 67. The polynucleotide of claim 66, wherein said heterologous polypeptide is a secretory signal peptide.

68. The polynucleotide of claim 67, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

10

69. The polynucleotide of any one of claims 56-68, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

70. The polynucleotide of any one of claims 56-68, which is RNA.

15

71. The polynucleotide of claim 70, which is messenger RNA (mRNA).

72. A vector comprising the polynucleotide of any one of claims 56-69.

20

73. The vector of claim 72, which is a plasmid.

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74. A composition comprising the polynucleotide of any one of claims 56-71, and a carrier.

75. The composition of claim 74, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating compound.

76. The composition of claim 75, wherein said adjuvant is selected from the group consisting of:

(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid; a cytokine; mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM); a solubilized mono-phosphoryl lipid A formulation; and CRL1005/BAK.

77. The composition of claim 76, wherein said adjuvant comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE), 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and

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1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

78. The composition of claim 77, wherein said neutral lipid is DPyPE.

5

79. The composition of claim 75, comprising the transfection facilitating compound (\pm)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

10 80. A method to treat or prevent anthrax infection in a vertebrate comprising: administering to a vertebrate in need thereof the composition of any one of claims 74-79.

15 81. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 50 contiguous amino acids of SEQ ID NO:12, wherein said nucleic acid fragment is a portion of an optimized coding region for the polypeptide of SEQ ID NO:12;

wherein about 13 of the 29 phenylalanine codons in said coding region are TTT and about 16 of said phenylalanine codons are TTC;

20 wherein about 6 of the 80 leucine codons in said coding region are TTA, about 10 of said leucine codons are TTG, about 10 of said leucine codons are CTT, about 16 of said leucine codons are CTC, about 6 of said leucine codons are CTA, and about 32 of said leucine codons are CTG;

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wherein about 26 of the 74 isoleucine codons in said coding region are ATT, about 36 of said isoleucine codons are ATC, and about 12 of said isoleucine codons are ATA;

wherein the 10 methionine codons in said coding region are ATG;

5 wherein about 7 of the 40 valine codons in said coding region are GTT, about 9 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 19 of said valine codons are GTG;

wherein about 10 of the 54 serine codons in said coding region are TCT, about 12 of said serine codons are TCC, about 8 of said serine codons are TCA, about 3 of said serine codons are TCG, about 8 of said serine codons are AGT, and about 13 of said serine codons are AGC;

wherein about 6 of the 21 proline codons in said coding region are CCT, about 7 of said proline codons are CCC, about 6 of said proline codons are CCA, and about 2 of said proline codons are CCG;

15 wherein about 7 of the 28 threonine codons in said coding region are ACT, about 10 of said threonine codons are ACC, about 8 of said threonine codons are ACA, and about 3 of said threonine codons are ACG;

wherein about 9 of the 34 alanine codons in said coding region are GGT, about 14 of said alanine codons are GCC, about 8 of said alanine codons are GCA, and about 3 of said alanine codons are GCG;

20 wherein about 15 of the 35 tyrosine codons in said coding region are TAT and about 20 of said tyrosine codons are TAC;

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wherein about 9 of the 21 histidine codons in said coding region are CAT and about 12 of said histidine codons are CAC;

wherein about 10 of the 41 glutamine codons in said coding region are CAA and about 31 of said glutamine codons are CAG;

5 wherein about 25 of the 54 asparagine codons in said coding region are AAT and about 29 of said asparagine codons are AAC;

wherein about 36 of the 86 lysine codons in said coding region are AAA and about 50 of said lysine codons are AAG;

10 wherein about 25 of the 55 aspartic acid codons in said coding region are GAT and about 30 of said aspartic acid codons are GAC;

wherein about 33 of the 79 glutamic acid codons in said coding region are GAA and about 46 of said glutamic acid codons are GAG;

wherein the single cysteine codon in said coding region is selected from the group consisting of TGT and TGC;

15 wherein the 5 tryptophan codons in said coding region are TGG;

wherein about 2 of the 27 arginine codons in said coding region are CGT, about 5 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 5 of said arginine codons are AGG; and

20 wherein about 6 of the 35 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 8 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

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82. The polynucleotide of claim 81, wherein said cysteine codon in said coding region is TGT.

5 83. The polynucleotide of claim 81, wherein said cysteine codon in said coding region is TGC.

84. The polynucleotide of claim 81, wherein said nucleic acid fragment encodes at least 100 contiguous amino acids of SEQ ID NO:12.

10 85. The polynucleotide of claim 84, wherein said nucleic acid fragment encodes amino acids 34 to 809 of SEQ ID NO:12.

86. The polynucleotide of claim 85, wherein said nucleic acid fragment comprises nucleotides 99 to 2427 of SEQ ID NO:26.

15

87. The polynucleotide of claim 81, wherein said nucleic acid fragment encodes amino acids 34-583 of SEQ ID NO:12.

20 88. The polynucleotide of claim 81, wherein said nucleic acid fragment encodes amino acids 34-254 of SEQ ID NO:12.

89. The polynucleotide of claim 81, wherein said nucleic acid fragment encodes amino acids 34-295 of SEQ ID NO:12.

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90. The polynucleotide of any one of claims 81-89, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

5 91. The polynucleotide of claim 90, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

10 92. The polynucleotide of claim 91, wherein said heterologous polypeptide is a secretory signal peptide.

93. The polynucleotide of claim 92, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

15 94. The polynucleotide of any one of claims 81-93, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

95. The polynucleotide of any one of claims 81-93, which is RNA.

20 96. The polynucleotide of claim 95, which is messenger RNA (mRNA).

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97. A vector comprising the polynucleotide of any one of claims 81-94.

98. The vector of claim 97, which is a plasmid.

5

99. A composition comprising the polynucleotide of any one of claims 81-96, and a carrier.

100. The composition of claim 99, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating compound.

10

101. The composition of claim 100, wherein said adjuvant is selected from the group consisting of:

15 (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;
a cytokine;
mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);
20 a solubilized mono-phosphoryl lipid A formulation; and
CRL1005/BAK.

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102. The composition of claim 101, wherein said adjuvant comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

- 5 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPB),
 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and
 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

103. The composition of claim 102, wherein said neutral lipid is
10 DPyPE.

104. The composition of claim 100, comprising the transfection facilitating compound (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

15

105. A method to treat or prevent anthrax infection in a vertebrate comprising: administering to a vertebrate in need thereof the composition of any one of claims 99-104.

20 106. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to amino acids 34 to 809 of SEQ ID NO:12, wherein said nucleic acid fragment is a variant fragment of an optimized coding region for the polypeptide of SEQ ID NO:12;

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wherein about 13 of the 29 phenylalanine codons in said coding region are TTT and about 16 of said phenylalanine codons are TTC;

wherein about 6 of the 80 leucine codons in said coding region are TTA, about 10 of said leucine codons are TTG, about 10 of said leucine
5 codons are CTT, about 16 of said leucine codons are CTC, about 6 of said leucine codons are CTA, and about 32 of said leucine codons are CTG;

wherein about 26 of the 74 isoleucine codons in said coding region are ATT, about 36 of said isoleucine codons are ATC, and about 12 of said isoleucine codons are ATA;

10 wherein the 10 methionine codons in said coding region are ATG;

wherein about 7 of the 40 valine codons in said coding region are GTT, about 9 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 19 of said valine codons are GTG;

wherein about 10 of the 54 serine codons in said coding region are
15 TCT, about 12 of said serine codons are TCC, about 8 of said serine codons are TCA, about 3 of said serine codons are TCG, about 8 of said serine codons are AGT, and about 13 of said serine codons are AGC;

wherein about 6 of the 21 proline codons in said coding region are CCT, about 7 of said proline codons are CCC, about 6 of said proline codons
20 are CCA, and about 2 of said proline codons are CCG;

wherein about 7 of the 28 threonine codons in said coding region are ACT, about 10 of said threonine codons are ACC, about 8 of said threonine codons are ACA, and about 3 of said threonine codons are ACG;

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wherein about 9 of the 34 alanine codons in said coding region are GGT, about 14 of said alanine codons are GCC, about 8 of said alanine codons are GCA, and about 3 of said alanine codons are GCG;

5 wherein about 15 of the 35 tyrosine codons in said coding region are TAT and about 20 of said tyrosine codons are TAC;

wherein about 9 of the 21 histidine codons in said coding region are CAT and about 12 of said histidine codons are CAC;

wherein about 10 of the 41 glutamine codons in said coding region are CAA and about 31 of said glutamine codons are CAG;

10 wherein about 25 of the 54 asparagine codons in said coding region are AAT and about 29 of said asparagine codons are AAC;

wherein about 36 of the 86 lysine codons in said coding region are AAA and about 50 of said lysine codons are AAG;

15 wherein about 25 of the 55 aspartic acid codons in said coding region are GAT and about 30 of said aspartic acid codons are GAC;

wherein about 33 of the 79 glutamic acid codons in said coding region are GAA and about 46 of said glutamic acid codons are GAG;

wherein the single cysteine codon in said coding region is selected from the group consisting of TGT and TGC;

20 wherein the 5 tryptophan codons in said coding region are TGG;

wherein about 2 of the 27 arginine codons in said coding region are CGT, about 5 of said arginine codons are CGC, about 3 of said arginine

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codons are CGA, about 6 of said arginine codons are CGG, about 6 of said
arginine codons are AGA, and about 5 of said arginine codons are AGG; and
wherein about 6 of the 35 glycine codons in said coding region are
GGT, about 12 of said glycine codons are GGC, about 8 of said glycine
5 codons are GGA, and about 9 of said glycine codons are GGG.

107. The polynucleotide of claim 106, wherein said cysteine codon
in said coding region is TGT.

10 108. The polynucleotide of claim 106, wherein said cysteine codon
in said coding region is TGC.

109. The polynucleotide of claim 106, wherein nucleic acid
fragment encodes a polypeptide at least 95% identical to amino acids 34 to
15 809 of SEQ ID NO:12.

110. The polynucleotide of claim 106, wherein the histidine codons
in said nucleic acid fragment corresponding to positions 719 and 723 of SEQ
ID NO:12 are deleted and each is replaced with a codon which codes for an
20 amino acid other than histidine, and wherein the glutamic acid codon in said
nucleic acid fragment corresponding to position 720 of SEQ ID NO:12 is
deleted and replaced with a codon which codes for an amino acid other than
glutamic acid.

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111. The polynucleotide of claim 110, wherein the histidine codons in said nucleic acid fragment corresponding to positions 719 and 723 of SEQ ID NO:12 are deleted and each is replaced with an alanine codon selected
5 from the group consisting of GCT, GCC, GCA, and GCG, and wherein the glutamic acid codon in said nucleic acid fragment corresponding to position 720 of SEQ ID NO:12 is deleted and replaced with an aspartic acid codon selected from the group consisting of GAT and GAC.

10 112. The polynucleotide of claim 111, which comprises nucleotides 82 to 2409 of SEQ ID NO:9.

113. The polynucleotide of claim 106, wherein the asparagine codons in said nucleic acid fragment corresponding to positions 62, 212, 286,
15 478, 712, 736, and 757 of SEQ ID NO:12 are deleted and each is replaced with a codon which codes for an amino acid other than asparagine.

114. The polynucleotide of claim 113, wherein the asparagine codons in said nucleic acid fragment corresponding to positions 62, 212, 286,
20 478, 712, 736, and 757 of SEQ ID NO:12 are deleted and each is replaced with a glutamine codon selected from the group consisting of CAA and CAG.

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115. The polynucleotide of claim 110, wherein the asparagine codons in said nucleic acid fragment corresponding to positions 62, 212, 286, 478, 712, 736, and 757 of SEQ ID NO:12 are deleted and each is replaced with a codon which codes for an amino acid other than asparagine.

5

116. The polynucleotide of claim 115, wherein the asparagine codons in said nucleic acid fragment corresponding to positions 62, 212, 286, 478, 712, 736, and 757 of SEQ ID NO:12 are deleted and each is replaced with a glutamine codon selected from the group consisting of CAA and CAG.

10

117. The polynucleotide of claim 116, wherein said glutamine codon is CAA.

118. The polynucleotide of claim 116, wherein said glutamine codon is CAG.

15

119. The polynucleotide of claim 116, which comprises nucleotides 82 to 2409 of SEQ ID NO:19.

120. The polynucleotide of any one of claims 106-119, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

20

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121. The polynucleotide of claim 120, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

5 122. The polynucleotide of claim 121, wherein said heterologous polypeptide is a secretory signal peptide.

123. The polynucleotide of claim 122, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

10

124. The polynucleotide of any one of claims 106-123, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

15 125. The polynucleotide of any one of claims 106-123, which is RNA.

126. The polynucleotide of claim 125, which is messenger RNA (mRNA).

20

127. A vector comprising the polynucleotide of any one of claims 106-124.

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128. The vector of claim 127, which is a plasmid.

129. A composition comprising the polynucleotide of any one of claims 106-126, and a carrier.

5

130. The composition of claim 129, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating compound.

10

131. The composition of claim 130, wherein said adjuvant is selected from the group consisting of:

(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

a cytokine;

15

mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

a solubilized mono-phosphoryl lipid A formulation; and

CRL1005/BAK.

20

132. The composition of claim 131, wherein said adjuvant comprises (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

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1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE),
1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and
1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

5 133. The composition of claim 132, wherein said neutral lipid is
DPyPE.

134. The composition of claim 130, comprising the transfection
facilitating compound (\pm)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-
10 bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

135. A method to treat or prevent anthrax infection in a vertebrate
comprising: administering to a vertebrate in need thereof the composition of
any one of claims 129-134.

15

Figure 1A

```

1  gatatcgcca ccatggatgc aatgaagaga gggctctgct gtgtgctgct gctgtgtgga
    m d a m k r g l c c v l l l c g

61  gcagtottcg tttcgcccag cagcgctggg ccaactgtgc ccgacagaga caatgatgga
    a v f v s p s s a g p t v p d r d n d g

121 atocctgata gtctagaggc tgagggatac acggtagatg tcaagaacaa aaggactttt
    i p d s l e v e g y t v d v k n k r t f

181 ctctcgcott ggatctcaaa tatccatgag aagaaggggc ttaccaagta caagtcctcc
    l s p w i s n i h e k k g l t k y k s s

241 cccgagaagt ggtctacogc ttccgatoca tatagcgatt tcgagaaggt cacaggccgg
    p e k w s t a s d p y s d f e k v t g r

301 atcgataaaa atgtgtctcc agaggctaga caccctctgg tagcagccta cccgattgta
    i d k n v s p e a r h p l v a a y p i v

361 cacgtggaca tggagaacat cattctaagc aaaaaogagg accagtccac acaaaacact
    h v d m e n i i l s k n e d q s t q n t

421 gactccgaga cccgcaccat atctaaaaac accagtactt caaggacca cacctctgaa
    d s e t r t i s k n t s t s r t h t s e

481 gtgcacggca atgcggaagt ccatgcacgc tttttcgata ttggtggctc cgtgtcagcc
    v h g n a e v h a s f f d i g g s v s a

541 ggcttttagca atagcaactc ctgcacgggt gccattgacc actcactgtc attagcaggt
    g f s n s n s s t v a i d h s l s l a g

601 gagaggactt gggctgaaac tatgggtotg aataccgccg atacggcccg gctcaacgca
    e r t w a e t m g l n t a d t a r l n a

661 aatatctcgt acgtcaacac agggactgct cctatatata acgtgctgcc taogacaagt
    n i r y v n t g t a p i y n v l p t t s

721 cttgtcctgg gcaaaaatca gaccctcgca accattaagg caaaggaaaa tcagctgagc
    l v l g k n q t l a t i k a k e n q l s

781 cagatcctcg ccctaacaa ctattatcca tccaaaaatt tagcccccac agccctgaac
    q i l a p n n y y p s k n l a p i a l n

841 gcccaggacg acttttctct taccctcata actatgaatt acaatcagtt cctggagctg
    a q d d f s s t p i t m n y n q f l e l

901 gaaaagacga agcagctgag actagacacc gatcaggtgt atggaaacat agcgacatat
    e k t k q l r l d t d q v y g n i a t y

961 aacttttgaga acggcccggt gcgcgtcgac actgggtcaa actggtctga agttctgccg
    n f e n g r v r v d t g s n w s e v l p

1021 caaattcaag agacaaccgc cagaattatc tttaatggga aggacttgaa cttgtcgaa
    q i q e t t a r i i f n g k d l n l v e

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Figure 1B

1081 cgtagaattg cgcgcgtgaa cccagtgat ccactcgaga cgactaaacc ggatatgaca
r r i a a v n p s d p l e t t k p d m t

1141 ctgaaagagg ctctgaagat tgccttcgga ttcaacgaac ctaatggcaa tttgcagtat
l k e a l k i a f g f n e p n g n l q y

1201 caggggaang acatcacaga gtttgatttc aatttcgatc agcagacttc ccaaaatata
q g k d i t e f d f n f d q q t s q n i

1261 aaaaatcagt tggcagagct gaatgccacc aatatctaca cggttctcga taaaatcaaa
k n q l a e l n a t n i y t v l d k i k

1321 cttaacgcca agatgaacat attgattcga gacaaacgct tccactacga cogcaacaat
l n a k m n i l i r d k r f h y d r n n

1381 atagccgtag gcgctgatga gtctgtcgtc aaggaggoto ataggggaagt tatcaacagc
i a v g a d e s v v k e a h r e v i n s

1441 agtactgaag ggctgttact taatatcgac aaggacattc ggaagatcct gtccgggtat
s t e g l l l n i d k d i r k i l s g y

1501 atcgtggaga tcgaggatac cgagggcctg aaggaagtca ttaacgaccg ctatgatatg
i v e i e d t e g l k e v i n d r y d m

1561 ctgaacattt ccagcttacg acaggacggt aagacattta ttgactttaa aaagtataac
l n i s s l r q d g k t f i d f k k y n

1621 gacaagctac ccctgtacat ttccaacca aattacaaag ttaatgtgta tgctgtaacc
d k l p l y i s n p n y k v n v y a v t

1681 aaggagaaca caatcatcaa tccaagogag aacggcgata ccagcacaaa tggaatcaaa
k e n t i i n p s e n g d t s t n g i k

1741 aagatcctta tatttagtaa aaaaggctac gagatcgggt gaggatcc
k i l i f s k k g y e i g -

Figure 2A

1 gatatcgcca ccatggatgc aatgaagaga gggctctgct gtgtgctgct gctgtgtgga gcagtcttcg
 m d a m k r g l c c v l l l c g a v f
 71 .tttcgccag cagcgctggg ccaactgtgc ccgacagaga caatgatgga atccctgata gtctagaggt
 v s p s s a g p t v p d r d n d g i p d s l e
 141 tgagggatac acggtagatg tcaagaacaa aaggactttt ctctcgccctt ggatctcaaa tatccatgag
 v e g y t v d v k n k r t f l s p w i s n i h e
 211 aagaaggggc ttaccaagta caagtcctcc cccgagaagt ggtctaccgc ttccgatcca tatagcgatt
 k k g l t k y k s s p e k w s t a s d p y s d
 281 tcgagaaggt cacaggccgg atcgataaaa atgtgtctcc agaggctaga caccctctgg tagcagccta
 f e k v t g r i d k n v s p e a r h p l v a a
 351 cccgattgta cacgtggaca tggagaacat cattctaagc aaaaacgagg accagtcac acaaaacact
 y p i v h v d m e n i i l s k n e d q s t q n t
 421 gactccgaga cccgcacat atctaaaaac accagtactt caaggaccca cacctctgaa gtgcacggca
 d s e t r t i s k n t s t s r t h t s e v h g
 491 atgcggaagt ccatgcatcg gatattgggt gctccgtgtc agccggcttt agcaatagca actcctcgac
 n a e v h a s d i g g s v s a g f s n s n s s
 561 ggttgccatt gaccactcac tgtcattagc aggtgagagg acttgggctg aaactatggg tctgaatacc
 t v a i d h s l s l a g e r t w a e t m g l n t
 631 gccgatacgg cccggctcaa cgcaaatatt cggtagctca acacagggac tgctcctata tataacgtgc
 a d t a r l n a n i r y v n t g t a p i y n v
 701 tgcctacgac aagtcttgtc ctgggcaaaa atcagaccct cgcaaccatt aaggcaaagg aaaattagct
 l p t t s l v l g k n q t l a t i k a k e n q
 771 gagccagatc ctgccccta acaactatta tccatccaaa aatttagccc ccatagccct gaacgccag
 l s q i l a p n n y y p s k n l a p i a l n a q
 841 gacgactttt cctctacccc cataactatg aattacaatc agttcctgga gctggaaaag acgaagcagc
 d d f s s t p i t m n y n q f l e l e k t k q
 911 tgagactaga caccgatcag gtgtatggaa acatagcgac atataacttt gagaacggcc gcgtgcgcgt
 l r l d t d q v y g n i a t y n f e n g r v r
 981 cgacactggg tcaaaactgg ctgaagttct gccgcaaatt caagagacaa ccgccagaat tatctttaat
 v d t g s n w s e v l p q i q e t t a r i i f n
 1051 ggggaaggact tgaaccttgt cgaacgtaga attgccgccc tgaaccccag tgatccactc gagacgacta
 g k d l n l v e r r i a a v n p s d p l e t t
 1121 aaccygatat gacactgaaa gaggtcttga agattgcctt cggattcaac gaacctaatg gcaatttgca
 k p d m t l k e a l k i a f g f n e p n g n l
 1191 gtatcagggg aaagacatca cagagtttga tttcaatttc gatcagcaga cttcccaaaa tatcaaaaat
 q y q g k d i t e f d f n f d q q t s q n i k n
 1261 cagttggcag agctgaatgc caccaatatc tacacggttc tcgataaaat caaacttaac gccaaagatga
 q l a e l n a t n i y t v l d k i k l n a k m
 1331 acatatgtat tcgagacaaa cgcttcact acgaccgcaa caatatagcc gtaggcgctg atgagtctgt
 n i l i r d k r f h y d r n n i a v g a d e s
 1401 cgtcaaggag gctcataggg aagttatcaa cagcagtact gaagggtgt tacttaatat cgacaaggac
 v v k e a h r e v i n s s t e g l l l n i d k d
 1471 attcgaaga tcctgtccgg gtatatcgtg gagatcgagg ataccgagg cctgaaggaa gtcattaacg
 i r k i l s g y i v e i e d t e g l k e v i n

Figure 2B

1541 accgctatga tatgctgaac atttccagct tacgacagga cggtaagaca tttattgact ttaaaaagta
d r y d m l n i s s l r q d g k t f i d f k k

1611 taacgacaag ctaccctgt acatttccaa cccaaattac aaagttaatg tgtatgctgt aaccaaggag
y n d k l p l y i s n p n y k v n v y a v t k e

1681 aacacaatca tcaatccaag cgagaacggc gataccagca caaatggaat caaaaagatc cttatattta
n t i i n p s e n g d t s t n g i k k i l i f

1751 gtaaaaaagg ctacgagatc gggtgaggat cc
s k k g y e i g -

Figure 3A

1 gatatcgcca ccatggatgc aatgaagaga gggctctgct gtgtgctgct gctgtgtgga
 m d a m k r g l c c v l l l c g
 61 gcagtcttcg tttcgccag cgaagtgaag caagaaaatc gacttctgaa cgagagcgaa
 a v f v s p s e v k q e n r l l n e s e
 121 agttcatcac agggctcttct cggatactac ttcagtgact tgaatttoca agcaccaatg
 s s s q g l l g y y f s d l n f q a p m
 181 gtgggtgacta gtagcaccac cggcgatttg agcattccca gctctgagtt ggagaacatt
 v v t s s t t g d l s i p s s e l e n i
 241 cccagcgaaa atcagtactt ccagtctgct atctggtccg gattcattaa ggttaaaaag
 p s e n q y f q s a i w s g f i k v k k
 301 tccgacgaat atacatttgc tacctcggcg gataaccatg tgacaatgtg ggtggacgac
 s d e y t f a t s a d n h v t m w v d d
 361 caggaagtga tcaacaaggc tttaaactct aataaaatcc ggctcgagaa ggggaggctc
 q e v i n k a s n s n k i r l e k g r l
 421 taccagatca aaattcagta ccagcgggaa aaccctacag aaaaaggact cgatttcaag
 y q i k i q y q r e n p t e k g l d f k
 481 ctgtactgga cagatagcca aaacaagaaa gaagttatca gctcagacaa tctgcagtta
 l y w t d s q n k k e v i s s d n l q l
 541 cccgagctca agcagaagag ttctaataca agcgctgggc caactgtgcc cgacagagac
 p e l k q k s s n t s a g p t v p d r d
 601 aatgatggaa tccctgatag tctagaggtt gagggataca cggtagatgt caagaacaaa
 n d g i p d s l e v e g y t v d v k n k
 661 aggacttttc tctcgcottg gatctoaat atccatgaga agaaggggct taccaagtac
 r t f l s p w i s n i h e k k g l t k y
 721 aagtcctccc ccgagaagtg gtctaccgct tccgatccat atagegattt cgagaaggct
 k s s p e k w s t a s d p y s d f e k v
 781 acaggccgga tcgataaaaa tgtgtctcca gaggctagac accccctggt agcagcctac
 t g r i d k n v s p e a r h p l v a a y
 841 ccgattgtac acgtggacat ggagaacatc attctaagca aaaacgagga ccagtccaca
 p i v h v d m e n i i l s k n e d q s t
 901 caaaacactg actccgagac ccgcaccata tctaaaaaca ccagtacttc aaggaccac
 q n t d s e t r t i s k n t s t s r t h
 961 acctctgaag tgcacggcaa tgcggaagtc catgcatcgt ttttcgatat tgggtggctcc
 t s e v h g n a e v h a s f f d i g g s
 1021 gtgtcagccg gcttttagcaa tagcaactcc tcgacggttg ccattgacca ctcaactgtca
 v s a g f s n s n s s t v a i d h e l s

Figure 3B

1081 ttagcaggtg agaggacttg ggctgaaact atgggtctga atacgcgga tacggcccg
 l a g e r t w a e t m g l n t a d t a r
 1141 ctcaacgcaa atattcggta cgtcaacaca gggactgctc ctatatataa cgtgctgcct
 l n a n i r y v n t g t a p i y n v l p
 1201 acgacaagtc ttgtcctggg caaaaatcag accctcgcaa ccattaaggc aaaggaaaat
 t t s l v l g k n q t l a t i k a k e n
 1261 cagctgagcc agatcctcgc ccctaacaac tattatccat ccaaaaattt agcccccata
 q l s q i l a p n n y y p s k n l a p i
 1321 gccctgaaog cccaggacga ctttctctct acccccataa ctatgaatta caatcagttc
 a l n a q d d f s s t p i t m n y n q f
 1381 ctggagctgg aaaagacgaa gcagctgaga ctagacaccg atcaggtgta tggaacata
 l e l e k t k q l r l d t d q v y g n i
 1441 gcgacatata aotttgagaa cggccgcgtg cgcgctcgaca ctgggtcaaa ctggtctgaa
 a t y n f e n g r v r v d t g s n w s e
 1501 gttctgccgc aaattcaaga gacaaccgcc agaattatct ttaatgggaa ggacttgaac
 v l p q i q e t t a r i i f n g k d l n
 1561 cttgtcgaac gtagaattgc ogcogtgaac cccagtgatc cactcgagac gactaaaccg
 l v e r r i a a v n p s d p l e t t k p
 1621 gatatgacac tgaaagaggc tctgaagatt gccttcggat tcaacgaacc taatggcaat
 d m t l k e a l k i a f g f n e p n g n
 1681 ttgcagtatc aggggaaaga catcacagag tttgatttca atttcgatca gcagacttcc
 l q y q g k d i t e f d f n f d q q t s
 1741 caaaatatca aaaatcagtt ggcagagctg aatgccacca atatctacac ggttctcgat
 q n i k n q l a e l n a t n i y t v l d
 1801 aaaatcaaac ttaacgcaa gatgaacata ttgattcgag acaaacgctt ccactacgac
 k i k l n a k m n i l i r d k r f h y d
 1861 cgcaacaata tagccgtagg cgctgatgag tctgtcgtca aggaggctca tagggaagtt
 r n n i a v g a d e s v v k e a h r e v
 1921 atcaacagca gtactgaagg gctgttactt aatatcgaca aggacattcg gaagatcctg
 i n s s t e g l l l n i d k d i r k i l
 1981 tccgggtata tcgtggagat cgaggatacc gagggcctga aggaagtcac taacgaccgc
 s g y i v e i e d t e g l k e v i n d r
 2041 tatgatatgc tgaacatttc cagcttacga caggacggta agacatttat tgactttaaa
 y d m l n i s s l r q d g k t f i d f k
 2101 aagtataacg acaagctacc cctgtacatt tccaacccaa attacaaagt taatgtgtat
 k y n d k l p l y i s n p n y k v n v y

Figure 3C

2161 gctgtaacca aggagaacac aatcatcaat ocaagcgaga acggcgatac cagcacaaat
a v t k e n t i i n p s e n g d t s t n

2221 ggaatcaaaa agatccttat atttagtaaa aaagggtacg agatcggttg aggatcc
g i k k i l i f s k k g y e i g -

1	gatatcgcca	ccatgggatgc	aatgaagaga	gggctctgct	gtgtgctgct	gotgtgtgga	
		m d	a m k r	g l c	c v l	l l c g	
61	gcagttcttcg	tttcgcccag	cgccggcggg	catggggacg	ttggcatgca	tgtgaaagaa	
	a v f	v s p	s a g g	h g d	v g m	h v k e	
121	aaggagaaaa	acaaggacga	aaacaagcgt	aaagacgaag	aacgtaataa	aacacaggag	
	k e k	n k d	e n k r	k d e	e r n	k t q e	
181	gaacacttaa	aggagatcat	gaagcacata	gtaaagattg	aggtaaaagg	cgaagaggct	
	e h l	k e i	m k h i	v k i	e v k	g e e a	
241	gtaaagaagg	aggcagcaga	aaaactgttg	gagaagggtgc	cttctgacgt	cttagagatg	
	v k k	e a a	e k l l	e k v	p s d	v l e m	
301	tataaggcca	tggcggttaa	gatctatatc	gtggacggag	acatcactaa	acacatatct	
	y k a	i g g	k i y i	v d g	d i t	k h i s	
361	ctcgaagctc	tctcogagga	caagaaaaag	attaaagaca	tctacgggaa	ggatgcctta	
	l e a	l s e	d k k k	i k d	i y g	k d a l	
421	ttgcacgagc	actacgttta	cgcaaaggag	ggctatgagc	ccgtgctcgt	tattcagagt	
	l h e	h y v	y a k e	g y e	p v l	v i q s	
481	agtgaggact	acgtcgagaa	taccgagaaa	gctctgaatg	tgtattacga	gatcggaaag	
	s e d	y v e	n t e k	a l n	v y y	e i g k	
541	attctgtccc	gggacatcct	gtccaaaatc	aaccagccat	aocagaaatt	ccttgatgtt	
	i l s	r d i	l s k i	n q p	y q k	f l d v	
601	cttaacacaa	tcaaaaacgc	gtcagatagc	gacgggcagg	atcttctgtt	tacaaatcaa	
	l n t	i k n	a s d s	d g q	d l l	f t n q	
661	ctcaaggaac	accccaactga	tttcagcgtg	gagttcctcg	agoagaattc	taacgaagtc	
	l k e	h p t	d f s v	e f l	e q n	s n e v	
721	caggaggtgt	tgcccaaggc	atttgogtac	tatatcgaac	cccagcatcg	cgatgtgctc	
	q e v	f a k	a f a y	y i e	p q h	r d v l	
781	cagctgtacg	ccccggaggc	atttaactac	atggacaaat	tcaatgaaca	ggagattaat	
	q l y	a p e	a f n y	m d k	f n e	q e i n	
841	ctgtctctgg	aggaactgaa	agaccagagg	atgctctccc	ggtatgaaaa	gtgggaaaaag	
	l s l	e e l	k d q r	m l s	r y e	k w e k	
901	atcaaacagc	attaccagca	ttgggtccgac	tccctgtcag	aagagggggc	cggcctgttg	
	i k q	h y q	h w s d	s l s	e e g	r g l l	
961	aaaaagtgtc	agattcccat	cgagcctaag	aaagatgata	taatacactc	tctaagccag	
	k k l	q i p	i e p k	k d d	i i h	s l s q	
1021	gaggagaagg	aactcctgaa	gcggatacaa	atcgactcat	ccgatttcct	tagcacagaa	
	e e k	e l l	k r i q	i d s	s d f	l s t e	

Figure 4B

1081 gagaaggagt ttctaaaaaa acttcagata gatattagag attcactgag cgaggaagag
 e k e f l k k l q i d i r d s l s e e e
 1141 aaggagctgc tcaaccgaat tcaagtcgat agttcgaacc ccttgtcaga aaaagagaag
 k e l l n r i q v d s s n p l s e k e k
 1201 gaattcctga aaaagttgaa gotcgacatc cagccgtacg atattaatca gcggctacaa
 e f l k k l k l d i q p y d i n q r l q
 1261 gacaccggcg gtctgattga tagccccagc atcaaccttg acgtacggaa gcaatataag
 d t g g l i d s p s i n l d v r k q y k
 1321 cgcgacattc aaaatatoga ogccctatta catcaatcca taggctccac gotataacaat
 r d i q n i d a l l h q s i g s t l y n
 1381 aaaatctatc tatacgaaaa catgaatatt aacaatctca ccgctacact gggagcggac
 k i y l y e n m n i n n l t a t l g a d
 1441 ctggctgata gtacagacaa cacaaagata aacagaggta ttttcaacga attcaaaaag
 l v d s t d n t k i n r g i f n e f k k
 1501 aactttaagt attcgatcag cagtaactat atgattgttg acatcaatga acggcccgcga
 n f k y s i s s n y m i v d i n e r p a
 1561 ttagacaatg agaggttgaa gtggagaatt caactgagtc ctgataactag ggccgggotat
 l d n e r l k w r i q l s p d t r a g y
 1621 ctggagaacg ggaaactgat cttacagcga aacatcgggc tggagatcaa ggatgtgcag
 l e n g k l i l q r n i g l e i k d v q
 1681 attatcaagc agagcgaaaa agaatacatt cgcacgcagc coaagggtggt gcctaagtca
 i i k q s e k e y i r i d a k v v p k s
 1741 aagatcgata ccaagatcca ggaagctcag ctcaacatta accaggagtg gaataaagct
 k i d t k i q e a q l n i n q e w n k a
 1801 cttgggtotgc caaaatacac caaacttata acctttaatg tgcacaacag gtatgcctct
 l g l p k y t k l i t f n v h n r y a s
 1861 aatatcgctc agtcagcata cctgattctc aatgaatgga agaacaatat tcagtctgac
 n i v e s a y l i l n e w k n n i q s d
 1921 ctgatcaaga aggtcacgaa ttatctggtg gacggaaatg gcagattcgt gttcaccgac
 l i k k v t n y l v d g n g r f v f t d
 1981 ataactttgc caaacattgc cgagcaatac actcatcagg atgaaattta cgagcaagtc
 i t l p n i a e q y t h q d e i y e q v
 2041 cactccaaag gtctgtatgt tccagagtca agatcgattc tgctccatgg tccatccaaa
 h s k g l y v p e s r s i l l h g p s k
 2101 ggggttgagc ttcgaaacga ttctgaggga tttatcgctg actttggagc cgctgtggat
 g v e l r n d s e g f i a d f g a a v d

Figure 4C

2161 gactacgccg gatacctggt ggataagaat cagtctgata tcgtgacaaa tagcaaaaaa
d y a g y l l d k n q s d l v t n s k k

2221 ttcatagata ttttcaagga ggaagggagt aacctgactt cctatggcgc cacgaacgag
f i d i f k e e g s n l t s y g r t n e

2281 gctgaatttt ttgoggaagc ctttagactt atgcacagca ccgaccatgc tgaaagggtg
a e f f a e a f r l m h s t d h a e r l

2341 aaggtgcaaa agaatgcccc taaaaccttc cagttcataa atgaccagat caagttcatc
k v q k n a p k t f q f i n d q i k f i

2401 atcaactctt gaggatcc
i n s -

Figure 5A

1 gatatcgcca ccatggatgc aatgaagaga gggctctgct gtgtgctgct gctgtgtgga
 m d a m k r g l c c v l l l c g
 61 gcagtcttctg ttctgcccag cgccggcggg catggggacg ttggcatgca tgtgaaagaa
 a v f v s p s a g g h g d v g m h v k e
 121 aaggagaaaa acaaggacga aaacaagcgt aaagacgaag aacgtaataa aacacaggag
 k e k n k d e n k r k d e e r n k t q e
 181 gaacacttaa aggagatcat gaagcacata gtaaagattg aggtaaaagg cgaagaggct
 e h l k e i m k h i v k i e v k g e e a
 241 gtaaagaagg aggcagcaga aaaactgttg gagaagggtgc cttctgacgt cttagagatg
 v k k e a a e k l l e k v p s d v l e m
 301 tataaggcca tcggoggtaa gatctatatc gtggacggag acatcactaa acacatatct
 y k a i g g k i y i v d g d i t k h i s
 361 ctgaagctc tctccgagga caagaaaaag attaaagaca tctacgggaa ggatgcctta
 l e a l s e d k k k i k d i y g k d a l
 421 ttgcacgagc actacgttta cgcaaaggag ggctatgagc ccgtgotcgt tattcagagt
 l h e h y v y a k e g y e p v l v i q s
 481 agtgaggact acgtogagaa taccgagaaa gctctgaatg tgtattacga gatcggaaag
 s e d y v e n t e k a l n v y y e i g k
 541 attctgtccc gggacatcct gtccaaaatc aaccagccat accagaaatt ccttgatgtt
 i l s r d i l s k i n q p y q k f l d v
 601 cttaacacaa tcaaaaacgc gtcagatagc gacgggcagg atcttctgtt tacaatcaa
 l n t i k n a s d s d g q d l l f t n q
 661 ctcaaggaac accccactga ttctagcgtg gagttcctcg agcagaattc taacgaagtc
 l k e h p t d f s v e f l e q n s n e v
 721 caggaggtgt tcgccaaggc atttgcgtac tatatcgaac cccagcatcg cgatgtgctc
 q e v f a k a f a y y i e p q h r d v l
 781 cagctgtacg ccccgagggc atttaactac atggacaaat tcaatgaaca ggagattaat
 q l y a p e a f n y m d k f n e q e i n
 841 ctgtctctgg aggaactgaa agaccagagg atgctctccc ggtatgaaaa gtgggaaaag
 l s l e e l k d q r m l s r y e k w e k
 901 atcaaacagc attaccagca ttgggtccgac tccctgtcag aagaggggcg cggcctgttg
 i k q h y q h w s d s l s e e g r g l l
 961 aaaaagtgtg agattcccat cgagcctaag aaagatgata taatacactc tctaagccag
 k k l q i p i e p k k d d i i h s l s q
 1021 gaggagaagg aactcctgaa gcggatacaa atcgactcat ccgatttctc tagcacagaa
 e e k e l l k r i q i d s s d f l s t e

Figure 5B

1081 gagaaggagt ttctaaaaaa acttcagata gatattagag attcactgag cgaggaagag
 e k e f l k k l q i d i r d s l s e e e
 1141 aaggagctgc tcaaccgaat tcaagtcgat agttcgaacc ccttgtcaga aaaagagaag
 k e l l n r i q v d s s n p l s e k e k
 1201 gaattcctga aaaagttgaa gctcgacatc cagccgtacg atattaatca goggctacaa
 e f l k k l k l d i q p y d i n q r l q
 1261 gacacggcg gtctgattga tagcccccagc atcaaccttg acgtacggaa gcaatataag
 d t g g l i d s p s i n l d v r k q y k
 1321 cgcgacattc aaaatatcga cgccctatta catcaatcca taggctccac gctatacaat
 r d i q n i d a l l h q s i g s t l y n
 1381 aaaatctatc tatacgaaaa catgaatatt aacaatctca ccgctacaot gggagcggac
 k i y l y e n m n i n n l t a t l g a d
 1441 ctggctgata gtacagacaa cacaagata aacagaggta ttttcaacga attcaaaaag
 l v d s t d n t k i n r g i f n e f k k
 1501 aactttaagt attogatcag cagtaactat atgattgttg acatcaatga acggcccgca
 n f k y s i s s n y m i v d i n e r p a
 1561 ttagacaatg agaggttgaa gtggagaatt caactgagtc ctgatactag ggccggctat
 l d n e r l k w r i q l s p d t r a g y
 1621 ctggagaacg ggaaactgat cttacagcga aacatcgggc tggagatcaa ggatgtgcag
 l e n g k l i l q r n i g l e i k d v q
 1681 attatcaagc agagcgaaaa agaatacatt cgcacgcacg ccaagggtggt gtagggatcc
 i i k q s e k e y i r i d a k v v -

Figure 6

```

1  gatatcgcca ccatggatgc aatgaagaga gggctotgct gtgtgctgct gctgtgtgga
    m d a m k r g l c c v l l l c g

61  gcagtcttcg tttcgcccag cgccggcggg catggggacg ttggcatgca tgtgaaagaa
    a v f v s p s a g g h g d v g m h v k e

121 aaggagaaaa acaaggacga aaacaagcgt aaagacgaag aacgtaataa aacacaggag
    k e k n k d e n k r k d e e r n k t q e

181 gaacacttaa aggagatcat gaagcacata gtaaagattg aggtaaaagg cgaagaggct
    e h l k e i m k h i v k i e v k g e e a

241 gtaaagaagg aggcagcaga aaaactgttg gagaagggtgc cttctgacgt cttagagatg
    v k k e a a e k l l e k v p s d v l e m

301 tataaggcca tcggcggtaa gatctatata gtggacggag acatcactaa acacatatct
    y k a i g g k i y i v d g d i t k h i s

361 ctgaagctc tctccgagga caagaaaaag attaaagaca tctacgggaa ggatgcctta
    l e a l s e d k k k i k d i y g k d a l

421 ttgcacgagc actacgttta ogcaaaggag ggctatgagc ccgtgctcgt tattcagagt
    l h e h y v y a k e g y e p v l v i q s

481 agtgaggact acgtcgagaa taccgagaaa gctctgaatg tgtattacga gatcggaaag
    s e d y v e n t e k a l n v y y e i g k

541 attctgtccc gggacatcct gtccaaaatc aaccagccat accagaaatt ccttgatgtt
    i l s r d i l s k i n q p y q k f l d v

601 cttaacacaa tcaaaaacgc gtcagatagc gacgggcagg atcttctgtt tacaatatcaa
    l n t i k n a s d s d g q d l l f t n q

661 ctcaaggaac accccactga tttcagcgtg gagttcctcg agcagaattc taacgaagtc
    l k e h p t d f s v e f l e q n s n e v

721 caggaggtgt tcgccaaggc attttgagga tcc
    q e v f a k a f -

```

Figure 7A

1 gatatcgcca ccatggatgc aatgaagaga gggctctgct gtgtgctgct gctgtgtgga
 m d a m k r g l c c v l l l c g
 61 gcagtcttcg tttcgcocag cagogctggg ccaactgtgc ccgacagaga caatgatgga
 a v f v s p s s a g p t v p d r d n d g
 121 atccctgata gtctagaggt tgaggatcac acggtagatg tcaagaacaa aaggaotttt
 i p d s l e v e g y t v d v k n k r t f
 181 ctctcgcctt ggatctcaaa tatccatgag aagaaggggc ttaccaagta caagtcctco
 l s p w i s n i h e k k g l t k y k s s
 241 ccogagaagt ggtctaccgc ttccgatcca tatagcgatt tcgagaaggt cacaggccgg
 p e k w s t a s d p y s d f e k v t g r
 301 atcgataaac aggtgtctcc agaggctaga cccccctgg tagcagocata ccgattgta
 i d k q v s p e a r h p l v a a y p i v
 361 cacgtggaca tggagaacat cattctaagc aaaaacgagg accagtccac acaaaacact
 h v d m e n i i l s k n e d q s t q n t
 421 gactccgaga ccgcacccat atctaaacag accagtactt caaggaccca cactctgaa
 d s e t r t i s k q t s t s r t h t s e
 481 gtgcacggca atgoggaagt ccatgcatcg ttttctgata ttggtggctc cgtgtcagcc
 v h g n a e v h a s f f d i g g s v s a
 541 ggcttttagca atagccagtc ctgcagcgtt gccattgacc actcactgtc attagcaggt
 g f s n s q s s t v a i d h s l s l a g
 601 gagaggactt gggctgaaac tatgggtctg aataccgccg ataccggccg gctcaacgca
 e r t w a e t m g l n t a d t a r l n a
 661 aatattcggg acgtcaacac agggactgct cctatatata acgtgctgcc tacgacaagt
 n i r y v n t g t a p i y n v l p t t s
 721 cttgtcctgg gcaaacagca gaacctcgca accattaagg caaaggaaaa tcagctgagc
 l v l g k q q t l a t i k a k e n q l s
 781 cagatccctg cccctaacaa ctattatcca tcaaaaaatt tagcccccatt agccctgaac
 q i l a p n n y y p s k n l a p i a l n
 841 gccaggaagc acttttcctc taaccccata actatgaatt acaatcagtt cctggagctg
 a q d d f s s t p i t m n y n q f l e l
 901 gaaaagacga agcagctgag actagacacc gatcaggtgt atggaaacat agcgacatat
 e k t k q l r l d t d q v y g n i a t y
 961 aactttgaga acggccgcgt gcgogtcgac actgggtcac agtggctga agttctgccg
 n f e n g r v r v d t g s q w s e v l p
 1021 caaattcaag agacaaccgc cagaattatc tttaatggga aggacttgaa ccttgtcgaa
 q i q e t t a r i i f n g k d l n l v e

Figure 7B

1081 cgtagaattg ccgccgtgca goccagtgat ccactcgaga cgactaaacc ggatatgaca
 r r i a a v q p s d p l e t t k p d m t

1141 ctgaaagagg ctctgaagat tgccttcgga ttcaacgaac ctaatggcaa tttgcagtat
 l k e a l k i a f g f n e p n g n l q y

1201 caggggaaag acatcacaga gtttgatttc aatttcgato agcagacttc caaaaatatac
 q g k d i t e f d f n f d q q t s q n i

1261 aaaaatcagt tggcagagct gcaggccacc aatatctaca oggttctcga taaaatcaaa
 k n q l a e l q a t n i y t v l d k i k

1321 ottaacgccca agatgaacat attgattoga gacaaacgct tccactacga ccgcaacaat
 l n a k m n i l i r d k r f h y d r n n

1381 atagccgtag gcgctgatga gtctgtcgtc aaggaggctc ataggggaagt tatccagagc
 i a v g a d e s v v k e a h r e v i q s

1441 agtactgaag ggctgttact taatatcgac aaggacattc ggaagatcct gtcggggtat
 s t e g l l l n i d k d i r k i l s g y

1501 atcgtggaga tcgaggatac cgagggcctg aaggaagtca ttaacgaccg ctatgatatg
 i v e i e d t e g l k e v i n d r y d m

1561 ctgcagatatt ccagcttacg acaggaagggt aagacattta ttgactttaa aaagtataac
 l q i s s l r q d g k t f i d f k k y n

1621 gacaagctac ccctgtacat ttccaaccca aattacaaag ttaatgtgta tgctgtaacc
 d k l p l y i s n p n y k v n v y a v t

1681 aaggagaaca caatcatcca gccaaagcgag aacggcgata ccagcacaaa tggaatcaaa
 k e n t i i q p s e n g d t s t n g i k

1741 aagatcctta tatttagtaa aaaaggctac gagatcggtt gaggatcc
 k i l i f s k k g y e i g -

1	gatatcgcca	ccatgggatgc	aatgaagaga	gggctctgct	gtgtgctgct	gctgtgtgga
		m d	a m k r	g l c	c v l	l l c g
61	gcagtccttcg	tttcgcccag	cgocggcggg	oatggggag	ttggcatgca	tgtgaaagaa
	a v f	v s p	s a g g	h g d	v g m	h v k e
121	aaggagaaaa	acaaggacga	aaacaagcgt	aaagacgaag	aacgtcagaa	aacacaggag
	k e k	n k d	e n k r	k d e	e r q	k t q e
181	gaacacttaa	aggagatcat	gaagcacata	gtaaagattg	aggtaaaagg	cgaagaggct
	e h l	k e i	m k h i	v k i	e v k	g e e a
241	gtaaagaagg	aggcagcaga	aaaactgttg	gagaagggtgc	cttctgacgt	cttagagatg
	v k k	e a a	e k l l	e k v	p s d	v l e m
301	tataaggcca	tggcggttaa	gatctatatc	gtggacggag	acatcactaa	acacatatct
	y k a	i g g	k i y i	v d g	d i t	k h i s
361	ctcgaagctc	tctccgagga	caagaaaaag	attaaagaca	totacgggaa	ggatgcctta
	l e a	l s e	d k k k	i k d	i y g	k d a l
421	ttgcacgagc	actacgttta	cgcaaaggag	ggctatgagc	ccgtgctcgt	tattcagagt
	l h e	h y v	y a k e	g y e	p v l	v i q s
481	agtgaggact	acgtcgagaa	taccgagaaa	gctctgaatg	tgtattacga	gatcggaaaag
	s e d	y v e	n t e k	a l n	v y y	e i g k
541	attctgtccc	gggacatcct	gtccaaaatc	aaccagccat	accagaaatt	ccttgatgtt
	i l s	r d i	l s k i	n q p	y q k	f l d v
601	cttaacacaa	tcaaacaggc	gtcagatagc	gacgggcagg	atcttctgtt	tacaaatcaa
	l n t	i k q	a s d s	d g q	d l l	f t n q
661	ctcaaggaac	accccaactga	tttcagcgtg	gagttcctcg	agcagaattc	taacgaagtc
	l k e	h p t	d f s v	e f l	e q n	s n e v
721	caggaggtgt	tgcccaaggc	atttgcgtac	tatatcgaac	cccagcatcg	cgatgtgctc
	q e v	f a k	a f a y	y i e	p q h	r d v l
781	cagctgtacg	ccccggaggc	atttaactac	atggacaaat	tcaatgaaca	ggagattcag
	q l y	a p e	a f n y	m d k	f n e	q e i q
841	ctgtctctgg	aggaactgaa	agaccagagg	atgctctccc	ggtatgaaaa	gtgggaaaaag
	l s l	e e l	k d q r	m l s	r y e	k w e k
901	atcaaacagc	attaccagca	ttggtccgac	tccctgtcag	aagagggggc	cggcctgttg
	i k q	h y q	h w s d	s l s	e e g	r g l l
961	aaaaagttgc	agattcccat	cgagcctaag	aaagatgata	taatacactc	tctaagccag
	k k l	q i p	i e p k	k d d	i i h	s l s q
1021	gaggagaagg	aactcctgaa	gcggatacaa	atcgactcat	ccgatttcct	tagcacagaa
	e e k	e l l	k r i q	i d s	s d f	l s t

Figure 8B

1081 gagaaggagt ttctaaaaaa acttcagata gatattagag attcactgag cgaggaagag
 e k e f l k k l q i d i r d s l s e e e
 1141 aaggagctgc tcaacogaat tcaagtcgat agttcgaacc ccttgtcaga aaaagagaag
 k e l l n r i q v d s s n p l s e k e k
 1201 gaattcctga aaaagttgaa gctcgacatc cagccgtacg atattaatoa ggggctacaa
 e f l k k l k l d i q p y d i n q r l q
 1261 gacaccggcg gtctgattga tagccccagc atcaaccttg acgtacggaa gcaatataag
 d t g g l i d s p s i n l d v r k q y k
 1321 cgcgacattc aaaatatcga cgccctatta catcaatcca taggctccac gctatacaat
 r d i q n i d a l l h q s i g s t l y n
 1381 aaaatctatc tatacgaaaa catgaatatt aaccagctca ccgctacact gggagcggac
 k i y l y e n m n i n q l t a t l g a d
 1441 ctggctgata gtacagacaa cacaagata aacagaggta ttttcaacga attcaaaaag
 l v d s t d n t k i n r g i f n. e f k k
 1501 aactttaagt attcgatcag cagtaactat atgattgttg acatcaatga acggcccgca
 n f k y s i s s n y m i v d i n e r p a
 1561 ttagacaatg agagggtgaa gtggagaatt caactgagtc ctgatactag ggccggctat
 l d n e r l k w r i q. l s p d t r a g y
 1621 ctggagaacg ggaaactgat cttacagcga aacatcgggc tggagatcaa ggatgtgcag
 l e n g k l i l q r n i g l e i k d v q
 1681 attatcaagc agagcgaaaa agaatacatt cgcacgcacg ccaagggtggg gcctaagtca
 i i k q s e k e y i r i d a k v v p k s
 1741 aagatcgata ccaagatcca ggaagctcag ctcaacatta accaggagtg gaataaagct
 k i d t k i q e a q l n i n q e w n k a
 1801 cttggctctgc caaaatacac caaacttctc acctttaatg tgcacaacag gtatgcctct
 l g l p k y t k l i t f n v h n r y a s
 1861 aatatcgctg agtcagcata cctgattctc aatgaatgga agaacaatat tcagtctgac
 n i v e s a y l i l n e w k n n i q s d
 1921 ctgatcaaga aggtcacgaa ttatctgggtg gacggaaatg gcagattcgt gttcaccgac
 l i k k v t n y l v d g n g r f v f t d
 1981 ataactttgc caaacattgc cgagcaatac actcatcagg atgaaattta cgagcaagtc
 i t l p n i a e q y t h q d e i y e q v
 2041 cactccaaag gtctgtatgt tccagagtca agatcgattc tgctccatgg tccatccaaa
 h s k g l y v p e s r s i l l h g p s k
 2101 gggggttgagc ttcgacagga ttctgaggga tttatcgctg actttggagc cgctgtggat
 g v e l r q d s e g f i a d f g a a v d

Figure 8C

2161 gactacgccg gatacctggt ggataagcag cagtctgatc tcgtgacaaa tagcaaaaaa
d y a g y l l d k q q s d l v t n s k k

2221 ttcataagata ttttcaagga ggaagggagt cagctgactt cctatggocg cacgaaogag
f i d i f k e e g s q l t s y g r t n e

2281 gotgaatttt ttgcggaagc ctttagactt atgcacagca ccgaccatgc tgaaagggttg
a e f f a e a f r l m h s t d h a e r l

2341 aaggtagcaaa agaattgcccc taaaaccttc cagttcataa atgaccagat caagttcatc
k v q k n a p k t f q f i n d q i k f i

2401 atcaactctt gaggatcc
i n s -

Figure 9A

TPA-Human PA	82	agcgctgggccaactgtgccgacagagacaatgatggaatccctgatagtctagaggttgaggatata
B.a.- PA	595	.t....a..t..g..t..a...c.t.....tcat.....a..a....t.
TPA-Human PA	152	cggtagatgtcaagaacaaaaggacttttctctcgccttgatctcaaatatccatgagaagaaggggct
B.a.- PA	665t.....a..t.....a.....t..a..a....t..t....t.....a.....a..at.
TPA-Human PA	222	taccaagtacaagtcctccccgagaagtggctaccgcttccgatccatatacggaatttcgagaaggtc
B.a.- PA	735	a.....a..t..a..a..t..t..a..a...agc..g....t....g..c..t.....a.....t
TPA-Human PA	292	acaggccggatcgataaaaatgtgtctccagaggctagacaccccctggtagcgcctaccgattgtac
B.a.- PA	805a.....t....g....a..a.....a.....t..g....t..t.....
TPA-Human PA	362	acgtggacatggagaacatcattctaagcaaaaacgaggaccagtcacacaaaacactgactccgagac
B.a.- PA	875	.t..a..t.....t..t.....ctca.....t....t..a.....g..t....tagt..a..
TPA-Human PA	432	ccgcaccatatctaaaaacaccagtaacttcaaggacccacacctctgaagtgcacggcaatgcggaagtc
B.a.- PA	945	ga..a..a...ag.....t..ttc...aagt....a..t..tag.....a..t..a.....a....g
TPA-Human PA	502	catgcatcgtttttcgataattggtggctccgtgtcagccggttttagcaatgaactcctcgacgggtg
B.a.- PA	1015g....c..t.....gagt..a..t..a..a....t....tcg..t..aagt....c.
TPA-Human PA	572	ccattgaccactcactgtcattagcagggtgagaggacttgggctgaaactatgggtctgaataccgccga
B.a.- PA	1085	.a.....t..t.....a..tc.....g..a.....a.....a.....t..a.....t..
TPA-Human PA	642	tacggcccggtcaacgcaaatattcggtacgtcaacacagggactgctcctatatataacgtgctgcct
B.a.- PA	1155	...a..aa.at..a..t..c.....a..t..a..t..t....g....a..c..c.....t..a..a
TPA-Human PA	712	acgacaagtcttgtcctgggcaaaaatcagaccctcgcaaccatttaaggcaaggaaaaatcagctgagcc
B.a.- PA	1225ttcgt..a..gt..a..a.....a..a.....g..a.....a..t.....c..at..a..t.
TPA-Human PA	782	agatcctcgccctaacaactattatccatccaaaaatttagcccccatagcctgaacgccaggacga
B.a.- PA	1295	.a..a..t..a.....t..t.....t..t.....c..g..g..a..c..at..a..t..a..a....
TPA-Human PA	852	cttttcctctacccccataactatgaattacaatcagttcctggagctggaaagacgaagcagctgaga
B.a.- PA	1365	t..cagt....t..a..t..a.....a..t..t..t..a.....a.....a..at..a...
TPA-Human PA	922	ctagacaccgatcagggtgtatggaaacatagcgacatataactttgagaacggccgctgcgctcgaca
B.a.- PA	1435	t....t..g....a..a.....g..t....a.....c..t....a..t..aa..a..a..g..g..t.
TPA-Human PA	992	ctgggtcaaaactgggtctgaagttctgcccgaattcaagagacaaccgccagaattatctttaatgggaa
B.a.- PA	1505	.a..c..g.....ag.....gt..a.....a.....a.....t..ac..t..c..t.....a..
TPA-Human PA	1062	ggacttgaacctgtgcgaacgtagaattgccgccgtgaacccagtgatccactcgagacgactaaaccg
B.a.- PA	1575	a..t..a..t..g..a...a..gc..g..a..g..g..t..t..t.....t..a..a.....
TPA-Human PA	1132	gatatgacactgaaagaggctctgaagattgccttcggattcaacgaacctaatggcaatttcagtatc
B.a.- PA	1645t..a.....a..c..t..a..a..a..t....t.....g....a..c..a..a....
TPA-Human PA	1202	aggggaagacatcacagagtttgatttcaatttcgatcagcagacttccaaaatatcaaaaatcagtt
B.a.- PA	1715	.a.....a.....a..c..a.....t.....a..a..a..t.....g.....
TPA-Human PA	1272	ggcagagctgaatgccaccaatatctacacgggtctcgataaaatcaaaacttaacgccaagatgaacata
B.a.- PA	1785	a..g..at..a..c..a..t..c..a..t..t..at..a.....t..a..t..a..a.....t..t
TPA-Human PA	1342	ttgattcgagacaaacgcttccactacgacgcaacaatatagccgtaggcgctgatgagtctgtcgtca
B.a.- PA	1855	..a..aa....t....t..t..t..t..ta..a..t..c....a..t..g..g.....a..a..t.
TPA-Human PA	1412	aggaggctcatagggaagttatcaacagcagttactgaagggtgttacttaatatcgacaaggacattcg
B.a.- PA	1925a.....a..t..ttcgtca..a..g..at..a..gt..a.....t..t....t..aa.
TPA-Human PA	1482	gaagatcctgtccgggtatatcgtggagatcgaggataccgagggcctgaagggaagtcattaacgaccgc
B.a.- PA	1995	a..a..at..a..a..t....t..a..a..t..a.....t..a..g..t..a.....t..a..t..a..a
TPA-Human PA	1552	tatgatgtgtgaacatttccagcttacgacaggacggtaagacatttattgacttttaaaagtataacg
B.a.- PA	2065t....t....t..t....g..a..t..a..a.....a..t.....a.....t.

Figure 9B

TPA-Human PA	1622	acaagctacccctgtacatttccaacccaattacaaagttaatgtgtatgctgtaaccaaggagacac
B.a.- PA	2135	.t..at....gt.a..t..aagt..t..c.....t..g..a.....a.....t..t..a..a.....
TPA-Human PA	1692	aatcatcaatccaagcgagaaacggcgataaccagcacaaatggaatcaaaaagatccttatatttagtaaa
B.a.- PA	2205	t..t..t.....t..t.....t..g.....t..t..c..c..g.....g..a..tt.a..c...tc....
TPA-Human PA	1762	aaaggctacgagatcggttga
B.a.- PA	2275t.....a..a.a.

Figure 10A

TPA-human fu	82	gaagtgaagcaagaaaatcgacttctgaacgagagcgaaagttcatcacagggtcttctc
B.a.- PA	88t..a..g..g..c..gt.at.a..t..atca...tcaagt..c.....gt.a..a
TPA-human fu	142	ggatactacttcagtgacttgaattccaagcaccaatgggtggtgactagtagcaccacc
B.a.- PA	148t..t.....t.....t.....C.....t..ctc.tct..t..a
TPA-human fu	202	ggcgatttgagcattccagctctgagttggagaacattcccagcgaaaatcagtacttc
B.a.- PA	208	..g.....atct.....t..t.....a..a..t....atcg.....c..a..t..t
TPA-human fu	262	cagtctgctatctggtccggattcattaaggttaaaaagtcgcgcaatatacatttgct
B.a.- PA	268	..a.....t.....a.....t..c..a.....g...agt..t.....
TPA-human fu	322	acctcggcggataaccatgtgacaatgtgggtggacgaccaggaagtgtacaacaaggct
B.a.- PA	328	..t..c..t.....t.....a.....a..t.....a.....t..t..a...
TPA-human fu	382	tcaaactctaataaaatccggctcgagaagggaggctctaccagatcaaaattcagtac
B.a.- PA	388	..t..t.....c.....a.at.a..a..a..a..at.a..t..a..a.....a..t
TPA-human fu	442	cagcgggaaaaccctacagaaaaaggactcgatttcaagctgtactggacagatagccaa
B.a.- PA	448	..a..a.....t.....t.....t.g.....t.....c...tct...
TPA-human fu	502	aacaagaaagaagttatcagctcagacaatctgcagttacccgagctcaagcagaagagt
B.a.- PA	508	..t..a.....g..ttctagt..t..ct.a..a..g..a..at.a..a..a..atc.
TPA-human fu	562	tctaa-----tacaagcgctgggccaactgtgccgacagagacaat
B.a.- PA	568	..g..ctcaagaaaaaagcgaag.....t.....a..t..g..t..a..c..t.....
TPA-human fu	604	gatggaatccctgatagtctagaggttgaggatacacggtagatgtcaagaacaaaagg
B.a.- PA	628tcat.....a..a.....t.....t.....a..t.....a
TPA-human fu	664	acttttctctcgccttggaatctcaaatatccatgagaagaaggggcttaccaggtacaag
B.a.- PA	688t..a..a.....t..t.....t.....a.....a..at.a.....a..t..a
TPA-human fu	724	tcctcccccgagaagtgggtctaccgcttccgatccatatagcgatttcgagaaggtcaca
B.a.- PA	748	..a..t..t..a..a..agc..g.....t.....g..c..t.....a.....t...
TPA-human fu	784	ggccggatcgataaaaatgtgtctccagaggctagacacccctggtagcagcctacccg
B.a.- PA	808	..a.....t.....g.....a..a.....a.....t..g.....t..t...
TPA-human fu	844	attgtacacgtggacatggagaacatcattctaagcaaaaacgaggaccagtccacacaa
B.a.- PA	868t..a..t.....t..t.....ctca.....t.....t..a.....g
TPA-human fu	904	aacactgactccgagacccgcaccatatctaaaaacaccagtacttcaaggacccacacc
B.a.- PA	928	..t.....tagt..a..ga.a..a..ag.....t..ttc...aagt.....a..t..t
TPA-human fu	964	tctgaagtgcacggcaatgcggaagtccatgcacgtttttcgatatattggtggctccgtg
B.a.- PA	988	ag.....a..t..a.....a.....g.....g.....C..t.....gagt..a
TPA-human fu	1024	tcagccggcttttagcaatagcaactcctcgacgggttgccattgaccactcactgtcatta
B.a.- PA	1048	..t..a..a.....t...tcg..t..aagt.....c..a.....t..t.....a..tc..
TPA-human fu	1084	gcaggtgagaggacttgggtgaaactatgggtctgaataccgccgatacggcccggtc
B.a.- PA	1108g..a..a.....a.....t.a.....t.....a..aa.at.a
TPA-human fu	1144	aacgcaaatattcgggtacgtcaacacagggactgctcctatatataacgtgctgectacg
B.a.- PA	1168	..t..c.....a..t..a..t..t.....g.....a..c..c.....t..a..a...
TPA-human fu	1204	acaagtcttgtcctgggcaaaaatcagaccctcgcaaccattaaggcgaaggaaaatcag
B.a.- PA	1228	..ttcgt.a..gt.a..a.....a..a.....g..a.....a..t.....c..a
TPA-human fu	1264	ctgagccagatcctcgccctaacaactattatccatccaaaaatttagccccatagcc
B.a.- PA	1288	t.a..t..a..a..t..a.....t..t.....t..t.....c..g..g..a..c..a
TPA-human fu	1324	ctgaacgcccaggacgacttttctctacccccataactatgaattacaatcagttcctg
B.a.- PA	1348	t.a..t..a..a.....t..cagt.....t..a..t..a.....a..t..t

Figura 10B

TPA-human fu	1384	gagctggaaaagacgaagcagctgagactagacaccgatcaggtgtatggaaacatagcg
B.a.- PA	1408	...t.a.....a.....a.at.a...t....t..g.....a..a.....g..t.....a
TPA-human fu	1444	acatataactttgagaacggccgcgtgcgcgtcgacactgggtcaaactggctgaagtt
B.a.- PA	1468c..t.....a..t..aa.a...a.g..g..t..a..c..g.....ag.....g
TPA-human fu	1504	ctgccgcaaattcaagagacaaccgccagaattatctttaatgggaaggacttgaacctt
B.a.- PA	1528	t.a.....a.....t..ac.t..c..t.....a..a..t..a..t..g
TPA-human fu	1564	gtcgaacgtagaattgccgcgtgaaccccgatgatccactcgagacgactaaaccggat
B.a.- PA	1588	..a...a.gc.g..a..g..g..t..t..t.....t.a..a.....
TPA-human fu	1624	atgacactgaaagaggctctgaagattgccttcggattcaacgaacctaattggcaatttg
B.a.- PA	1648t.a.....a..c..t..a..a..a..t.....t.....g:....a..c..a
TPA-human fu	1684	cagtatcaggggaaagacatcacagagtttgatttcaatttcgatcagcagacttcccaa
B.a.- PA	1708	..a.....a.....a..c..a.....t.....a..a..a..t...
TPA-human fu	1744	aatatcaaaaatcagttggcagagctgaatgccaccaatatctacacggttctcgataaa
B.a.- PA	1768g.....a..g..at.a..c..a..t..c..a..t..t..at.a.....
TPA-human fu	1804	atcaaacttaacgccaagatgaacatattgattcgagacaaacgcttcactacgaccgc
B.a.- PA	1828t.a..t..a..a.....t..t..a..aa.....t.....t..t..t..ta.a
TPA-human fu	1864	aacaatatagccgtaggcgctgatgagtctgtcgtcaaggaggctcatagggaagttatc
B.a.- PA	1888	..t..c.....a..t..g..g.....a..a..t.....a.....a..t
TPA-human fu	1924	aacagcagtactgaagggtgttacttaatatcgacaaggacattcggaagatcctgtcc
B.a.- PA	1948	..ttcgtca..a..g..at.a..gt.a.....t..t.....t..aa.a..a..at.a..a
TPA-human fu	1984	gggtatatcgtggagatcgaggataaccgagggcctgaaggaagtcattaacgaccgctat
B.a.- PA	2008	..t.....t..a..a..t..a.....t..a..g..t..a.....t..a..t..a..a...
TPA-human fu	2044	gatatgctgaacatttccagcttacgacaggacggtaagacatttattgactttaaaaag
B.a.- PA	2068t....t....t..t....g..a..t..a..a.....a..t.....a
TPA-human fu	2104	tataacgacaagctaccctgtacatttccaacccaattacaaagttaatgtgtatgct
B.a.- PA	2128t..t..at....gt.a..t..aagt..t..c.....t..g..a.....a.....
TPA-human fu	2164	gtaaccaaggagaaacacaatcatcaatccaagcgagaacggcgataccagcacaatgga
B.a.- PA	2188	..t..t..a..a.....t..t..t....t..t....t..g....t..t..c..c..g
TPA-human fu	2224	atcaaaaagatccttatatttagtaaaaaaggctacgagatcggttgaggatcc
B.a.- PA	2248g..a..tt.a..c..tc.....t.....a..a..a-----

Figure 11A

TPA-Human LF	82	gccggcgggcatggggacgttgcatgcatgtgaaagaaaaggagaaaaacaaggacgaa
B.a.- LF	100	..g.....t.....t..t..a..t.....c..a.....g..a.....t..a..t..g
TPA-Human LF	142	aacaagcgtaaagacgaagaacgtaataaaacacaggaggaacacttaaggagatcatg
B.a.- LF	160	..t...a..a.....t.....a.....a.....a..g..t.....a.....
TPA-Human LF	202	aagcacatagtaaagattgaggtaaaaggcgaagaggctgtaaagaaggaggcagcagaa
B.a.- LF	220	..a.....t.....a..a..a.....g..g..a.....t..a..a.....
TPA-Human LF	262	aaactgttgagaaggtgccttctgacgtcttagagatgtataaggccatcggcggttaag
B.a.- LF	280	..g..ac..t.....a..a..a.....t..t.....a..a..t..a..a...
TPA-Human LF	322	atctatatcgtggacggagacatcactaaacacatatctctcgaagctctctccgaggac
B.a.- LF	340	..a.....t.....t..t..t..a.....t.....t..a.....at..a..t..a..t
TPA-Human LF	382	aagaaaaagattaaagacatctacgggaaggatgccttattgcacgagcactacgtttac
B.a.- LF	400a..a.....t..t.....a.....t.....a..t..a..t..t..a..t
TPA-Human LF	442	gcaaaggagggtatgagcccgctgctcgttattcagagtagtgaggactacgtcgagaat
B.a.- LF	460a..a..a.....a.....a..t..a..c..atc..tcg..a..t..t..a..a...
TPA-Human LF	502	accgagaaagctctgaatgtgtattacgagatcggaaagattctgtcccgggacatcctg
B.a.- LF	520	..t..a..g..a.....c..t.....t..a..a..t.....at..a..aa...t..tt..a
TPA-Human LF	562	tccaaaatcaaccagccataccagaaattccttgatgttcttaacacaatcaaaaacgcg
B.a.- LF	580	agt.....t..t..a.....t.....tt..a.....at..a..t..c..t.....t..a
TPA-Human LF	622	tcagatagcgacgggcaggatcttctgtttacaaatcaactcaaggaacaccccaactgat
B.a.- LF	640	..t...tca..t..a..a.....t..a.....t.....g..t.....t.....a..c
TPA-Human LF	682	ttcagcgtggagttcctcgagcagaattctaacgaagtcaggagggtgttcgccaaggca
B.a.- LF	700	..ttct..a..a...t..g..a..a...agc..t..g..a..a..a..a..t..g..a..t
TPA-Human LF	742	tttgcgtactatatcgaaacccagcatcgcatgtgctccagctgtacgccccggaggca
B.a.- LF	760a..t.....g..a.....t.....tt..a.....t..t..a.....a..t
TPA-Human LF	802	tttaactacatggacaaattcaatgaacaggagattaatctgtctctggaggaaactgaaa
B.a.- LF	820t.....t.....t..c.....a..a..a.....a..ct....a.....t...
TPA-Human LF	862	gaccagaggtatgctctcccgtatgaaaagtgggaaaagatcaaacagcattaccagcat
B.a.- LF	880	..t..ac.....g..aa..a.....a.....a.....c..t..a..c
TPA-Human LF	922	tggtccgactccctgtcagaagagggcgcgccctgttgaaaaagttgcagattcccatc
B.a.- LF	940	...ag...t..tt..a..t....a..aa..a..a..t..a.....c.....t..t
TPA-Human LF	982	gagcctaagaagatgatataatacactctctaagccaggaggagaaggaaactcctgaag
B.a.- LF	1000a.....c.....t..t..t..t..tct..a..a..a..a..g..t..a..a
TPA-Human LF	1042	cggatacaaatcgactcatccgatttccttagcacagaagagaaggagtttctaaaaaaa
B.a.- LF	1060	a.a.....t..tagtagt....tt.atct..t..g..a..a.....t.....g
TPA-Human LF	1102	cttcagatagatattagagattcactgagcgaggaagagaaggagctgtcaccggaatt
B.a.- LF	1120	..a..a..t.....c..t.....tt.atct..a.....a..a.....tt..a..ta....a
TPA-Human LF	1162	caagtcgatagttcgaacccttgtcagaaaaagagaaggaattcctgaaaaagttgaag
B.a.- LF	1180	..g..g.....agt..t..t..a..t.....a..a..g..tt..a.....c....a
TPA-Human LF	1222	ctcgacatccagccgtacgatattaatcagcggtacaagacacccggcggtctgattgat
B.a.- LF	1240	..t..t..t..a..a..t.....aa..t..g.....t..a..a..gt..a.....
TPA-Human LF	1282	agccccagcatcaaccttgacgtacggaagcaatataagcgacacattcaaatatcgac
B.a.- LF	1300	..t..gtca..t..t.....t..a..a.....g....aa..g..t.....t..t
TPA-Human LF	1342	gccctattacatcaatccataggtccacgctatacaataaaatctatctatacgaaaac
B.a.- LF	1360	..tt.....t..aagt..ct..g.....t..t..g..t.....t

Figure 11B

TPA-Human LF	1402	atgaatattaacaatctcacgctacactgggagcggacctggtcgatagtagacagacaac
B.a.- LF	1420C..t..C..t..a..a..C..a..t.....tt.a..t...tcc..t..t..t
TPA-Human LF	1462	acaaagataaacagagggtatcttcaacgaattcaaaaagaactttaagtattcgatcagc
B.a.- LF	1480	..t..a..t..t.....t.....a..t..c..a'..agt..ttct
TPA-Human LF	1522	agtaactatatgattgttgacatcaatgaacggcccgcatagacaatgagagggtgaag
B.a.- LF	1540t..a.....a....t.....t.....C.t.....a
TPA-Human LF	1582	tggagaattcaactgagtcctgatactagggccggctatctggagaacgggaaactgatc
B.a.- LF	1600C..t.atca..a.....C.a..a..a...t.a..a..t..a..g..t..a
TPA-Human LF	1642	ttacagcgaacatcgggctggagatcaaggatgtgcagattatcaagcagagcgaaaaa
B.a.- LF	1660aa.....t.....a..a.....a..a..a..t.....atc.....
TPA-Human LF	1702	gaatacattcgcacgcagcgaagggtggcctaagtcaaagatcgataccaagatccag
B.a.- LF	1720t..aa.g..t..t..g..a..a.....a...agt..a..a.....a..a..t..a
TPA-Human LF	1762	gaagctcagctcaacattaaccaggagtggaataaagctcttggctcgccaaaatacacc
B.a.- LF	1780a..t.a..t..a..t.....a.....at.a..gt.a.....t..a
TPA-Human LF	1822	aaacttatcacctttaatgtgcacaacagggtatgcctctaataatcgctcagtcagcatac
B.a.- LF	1840	..g.....t..a..C..C.....t..t..a.....a..C.....t..a..aagt..t..t
TPA-Human LF	1882	ctgattctcaatgaatggaagaacaatattcagtcctgacatgaagaagggtcacgaat
B.a.- LF	1900	t.a..at.g.....a..t.....aag...t..t..a..a.....a..a...
TPA-Human LF	1942	tatctggtggagcggaaatggcagattcgtgttcaccgacataactttgccaaacattgcc
B.a.- LF	1960	..ct.a..t..t..t.....a.....t..t..t.....t..t...c.C..t..t..a..t
TPA-Human LF	2002	gagcaatacactcatcaggatgaaatttacgagcaagtcactccaaagggtctgtatgtt
B.a.- LF	2020	..a.....t..a.....a.....g..a..t.....t..t..a.....gt.a.....
TPA-Human LF	2062	ccagagtcagatcgattctgctccatgggtccatccaaagggttgagcttcgaaacgat
B.a.- LF	2080a..cc.t..t..at.a.....a..t..a.....t..a..at.aa.g..t...
TPA-Human LF	2122	tctgagggtattatcgctgactttggagccgctgtggatgactacgccggatacctgttg
B.a.- LF	2140	ag.....t.....acac..a.....cat.....t..t..t.....t..a..a
TPA-Human LF	2182	gataagaatcagtcctgatctcgtgacaaatagcaaaaaattcatagatattttcaaggag
B.a.- LF	2200C..a.....t.a..t.....tct.....t.....t.....t.....a
TPA-Human LF	2242	gaagggtgaacctgacttcctatggccgcacgaacgaggctgaattttttgcggaagcc
B.a.- LF	2260tt.a.....g.....ga.a..a..t..a..g.....a.....
TPA-Human LF	2302	tttagacttatgcacagcaccgaccatgctgaaagggtgaagggtgcaaaagaatgccct
B.a.- LF	2320gt.a.....ttct..g.....c.t..a..a..t.....a.....t..g
TPA-Human LF	2362	aaaaccttcagttcataaatgaccagatcaagttcatcatcaactcttgaggatcc
B.a.- LF	2380t.....a..t..t..C..t.....t.....t..t.....a..a-----

Figure 12

TPA-Human PA	1	mdamkrglccvlllogavfvspsagptvpdrdndgipdslevegysvdknkrtflspw
Sugar minus	1
TPA-Human PA	61	isnihekkgltkykspekwtasdpysdfekvtgridknvspearhplvaayplvhvdm
Sugar minus	61q.....
TPA-Human PA	121	enilsknedqstqntdsetrtiskntsterthtsevhgnaevhasffdiggsvsagfsn
Sugar minus	121q.....
TPA-Human PA	181	snsstvaidslsislagertwaetmgintadtarlanniryvntgtapiynvlpttslvlg
Sugar minus	181	.q.....
TPA-Human PA	241	knqtlatikakenqlsqilapnnyypeknlapialnaqddfstpitmnynqflelektk
Sugar minus	241	.q.....
TPA-Human PA	301	qlrltdtdqvygniatynfengrvrvdtgsnwsevlpqiqettariifngkdlnlverria
Sugar minus	301q.....
TPA-Human PA	361	avnpsdplettkpdmtilkealkiafgfnepngnlqyqgkditfedfnfdqqtseqniknql
Sugar minus	361	..q.....
TPA-Human PA	421	aelnatniyvtldkiklnakmnilirdkrfhydrnniavgadesvvkeahrevinasteg
Sugar minus	421	...q.....q.....
TPA-Human PA	481	lllnidkdirkilegyiveiedteglkevindrydmnisslrqdgktfidfkkyndklp
Sugar minus	481q.....
TPA-Human PA	541	lyisnpykvnyvavtkentiinpsengdtstngikkilifskkgyeig
Sugar minus	541q.....

Figure 13

TPA-Human LF	1	mdamkrglccvlllccgavfvspagghgdvgmhvkkekaknkdkankrkdaernktqeehlk
Sugar minus	1q.....
TPA-Human LF	61	eimkhivkievkgeeavkkeaaekllekvpsdvlemykaiggkiyivdgditkhisleal
Sugar minus	61
TPA-Human LF	121	sedkkkikdiygkdallhehyvyakegyepvlviqssedyventekalnvyyeigkilsr
Sugar minus	121
TPA-Human LF	181	dilskinppygkfldvltiknaedsdgqdllftnqlkehptdfsvefleqnsnevqevf
Sugar minus	181q.....
TPA-Human LF	241	akafayyipqhrdvlqlyapeafnymdkfneqeinslealkdqrmlsryekwekikqh
Sugar minus	241q.....
TPA-Human LF	301	yqhwsdslseegrgllkklqipiepkddihslsgeekellkriqidssdfksteekf
Sugar minus	301
TPA-Human LF	361	lklqldirdslseeeekellnriqvdsenplsekekeflklklldiqpydingrlqdtgg
Sugar minus	361
TPA-Human LF	421	lidspsinldvrkqykrdignidallhqsigstlynkiylyenmninnltatlgadlvds
Sugar minus	421q.....
TPA-Human LF	481	tdntkinrgifnefkknfkysissnymivdinerpaldnerlkwriqlspdtragyleng
Sugar minus	481
TPA-Human LF	541	klilqrnigleikdvqiikqsekeyiridakvvpkskidtkigeaqlningewnkalglp
Sugar minus	541
TPA-Human LF	601	kytklitfnvhnryasnivesaylilnewknniqsdlikkvtnylvdgngrfvftditlp
Sugar minus	601
TPA-Human LF	661	niaeqythqdeiyevhskglyvpesrsilhgpskgvelrndsegfiadfgaavddyag
Sugar minus	661q.....
TPA-Human LF	721	ylldknqsdltvtnskkfidiifkeegsnltsygrtneaeffaeafrlmhstdhaerlkvqk
Sugar minus	721q.....q.....
TPA-Human LF	781	napktfqfindqikfiins
Sugar minus	781

Figure 14

1 gatatcgcca ccatggatgc aatgaagaga gggctctgct gtgtgctgct gctgtgtgga
 m d a m k r g l c c v l l l c g
 61 gcagtcttcg ttctgccag cgccggcggg catggggacg ttggcatgca tgtgaaagaa
 a v f v s p s a g g h g d v g m h v k e
 121 aaggagaaaa acaaggacga aaacaagcgt aaagacgaag aacgtaataa aacacaggag
 k e k n k d e n k r k d e e r n k t q e
 181 gaacacttaa aggagatcat gaagcacata gtaaagattg aggtaaaagg cgaagaggct
 e h l k e i m k h i v k i e v k g e e a
 241 gtaaagaagg aggcagcaga aaaactgttg gagaagggtc cttctgacgt cttagagatg
 v k k e a a e k l l e k v p s d v l e m
 301 tataaggcca tcggcggtaa gatctatatc gtggacggag acatcactaa acacatatct
 y k a i g g k i y i v d g d i t k h i s
 361 ctcaagctc tctccgagga caagaaaaag attaaagaca tctacgggaa ggatgcctta
 l e a l s e d k k k i k d i y g k d a l
 421 ttgcacgagc actacgttta cgcaaaggag ggctatgagc ccgtgctcgt tattcagagt
 l h e h y v y a k e g y e p v l v i q s
 481 agtgaggact acgtcgagaa taccgagaaa gctctgaatg tgtattacga gatcggaagg
 s e d y v e n t e k a l n v y y e i g k
 541 attctgtccc gggacatcet gtccaaaatc aaccagccat accagaaatt ccttgatgtt
 i l s r d i l s k i n q p y q k f l d v
 601 cttaacacaa tcaaaaacgc gtcagatagc gacgggcagg atcttctgtt tacaatatca
 l n t i k n a s d s d g q d l l f t n q
 661 ctcaaggaac accccactga ttctcagcgtg gagttcctcg agcagaattc taacgaagtc
 l k e h p t d f s v e f l e q n s n e v
 721 caggaggtgt tcgccaaggc atttgcgtac tatatcgaac ccagcatcg cgatgtgctc
 q e v f a k a f a y y i e p q h r d v l
 781 cagctgtacg ccccgagggc atttaactac atggacaaat tcaatgaaca ggagattaat
 q l y a p e a f n y m d k f n e q e i n
 841 ctgtctctgg aggaactgaa agaccagtga ggatcc
 l s l e e l k d q -

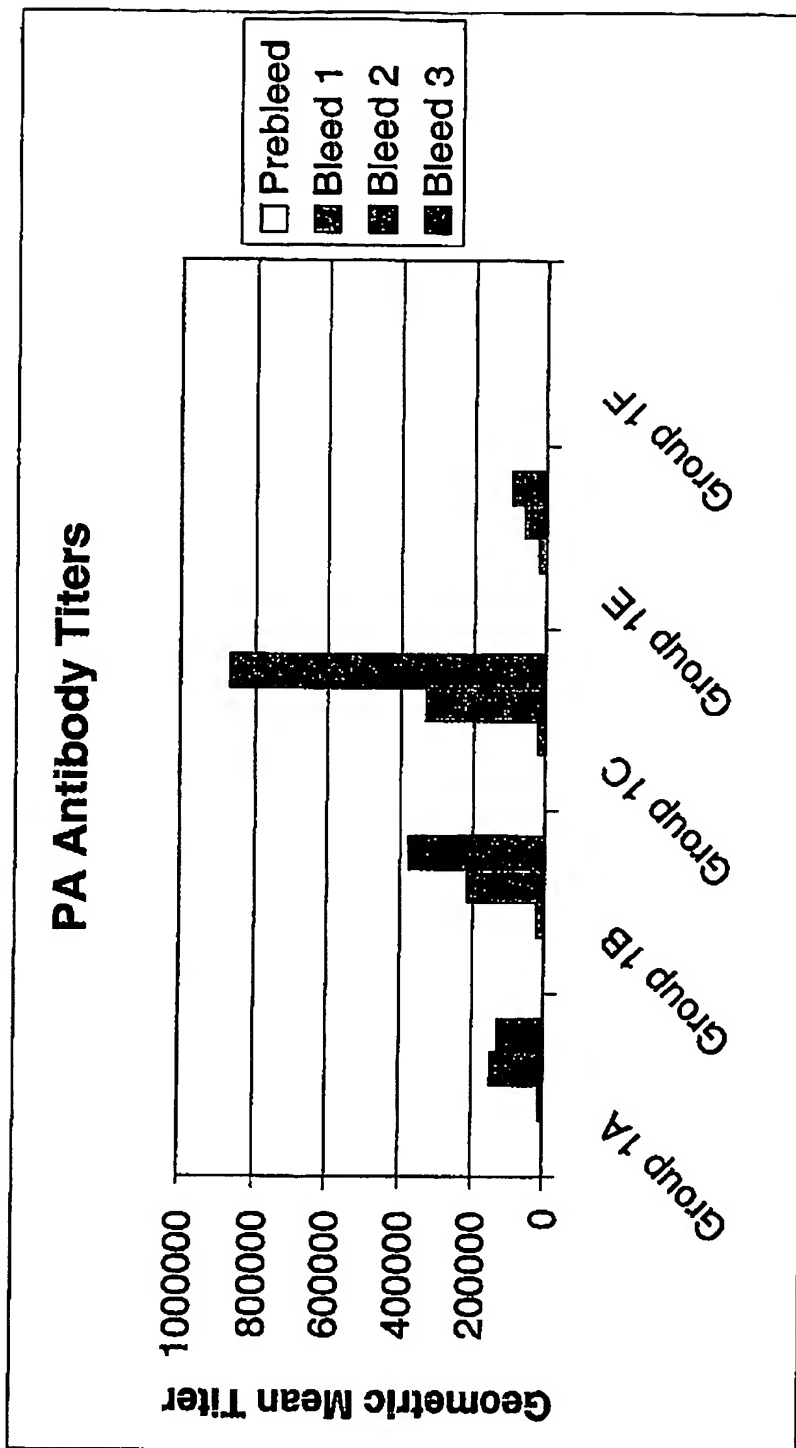


FIG. 15A

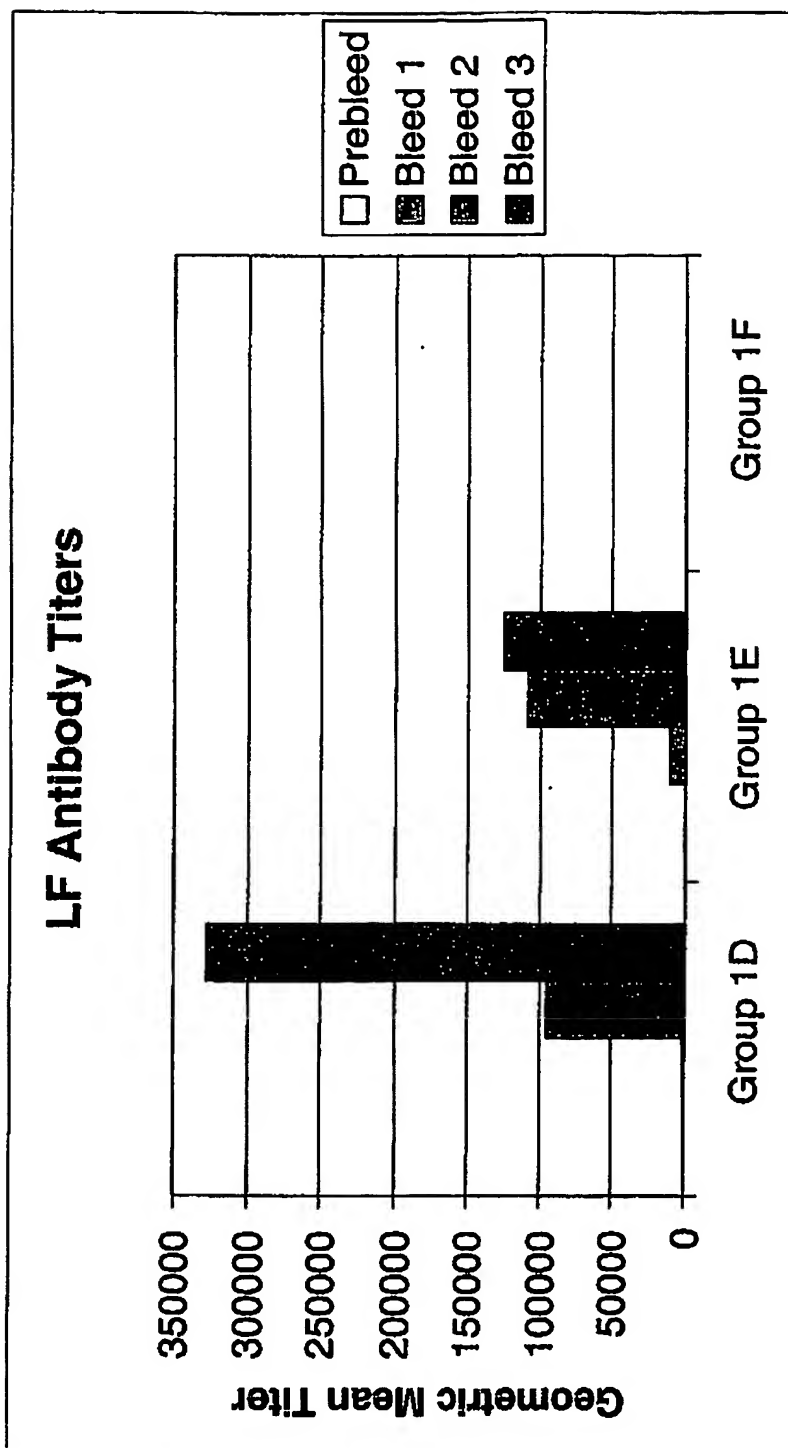


FIG. 15B

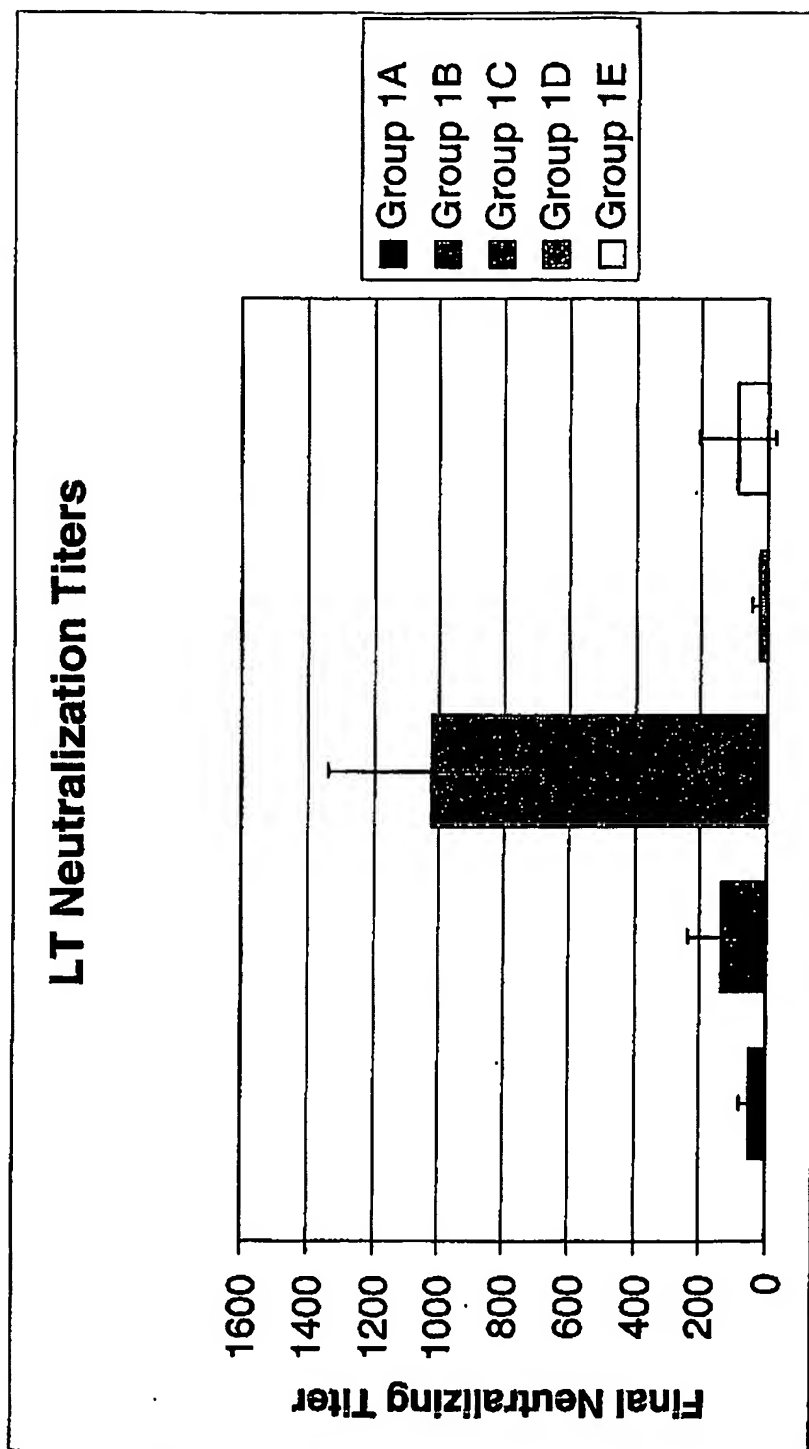


FIG. 15C

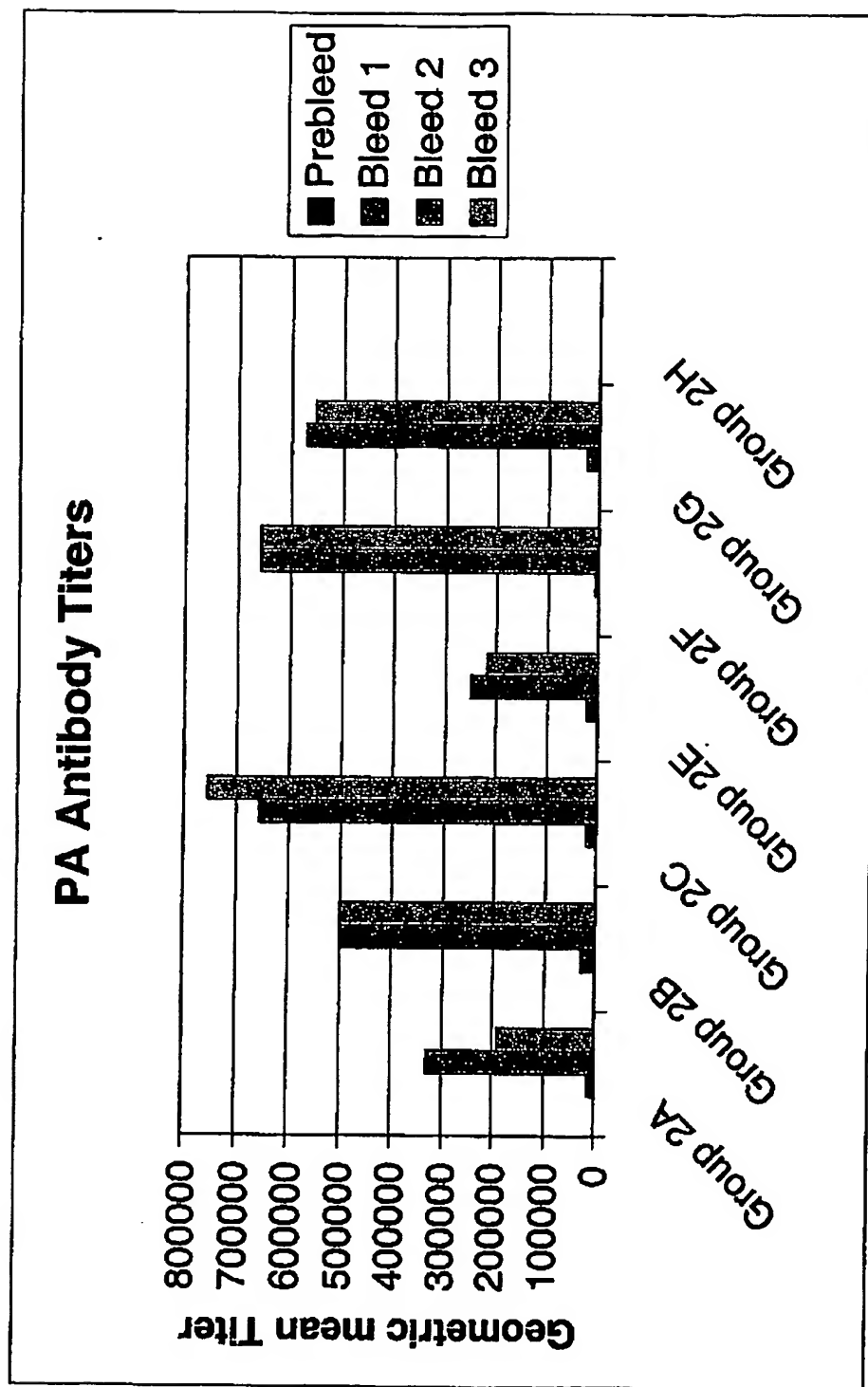


FIG. 16A

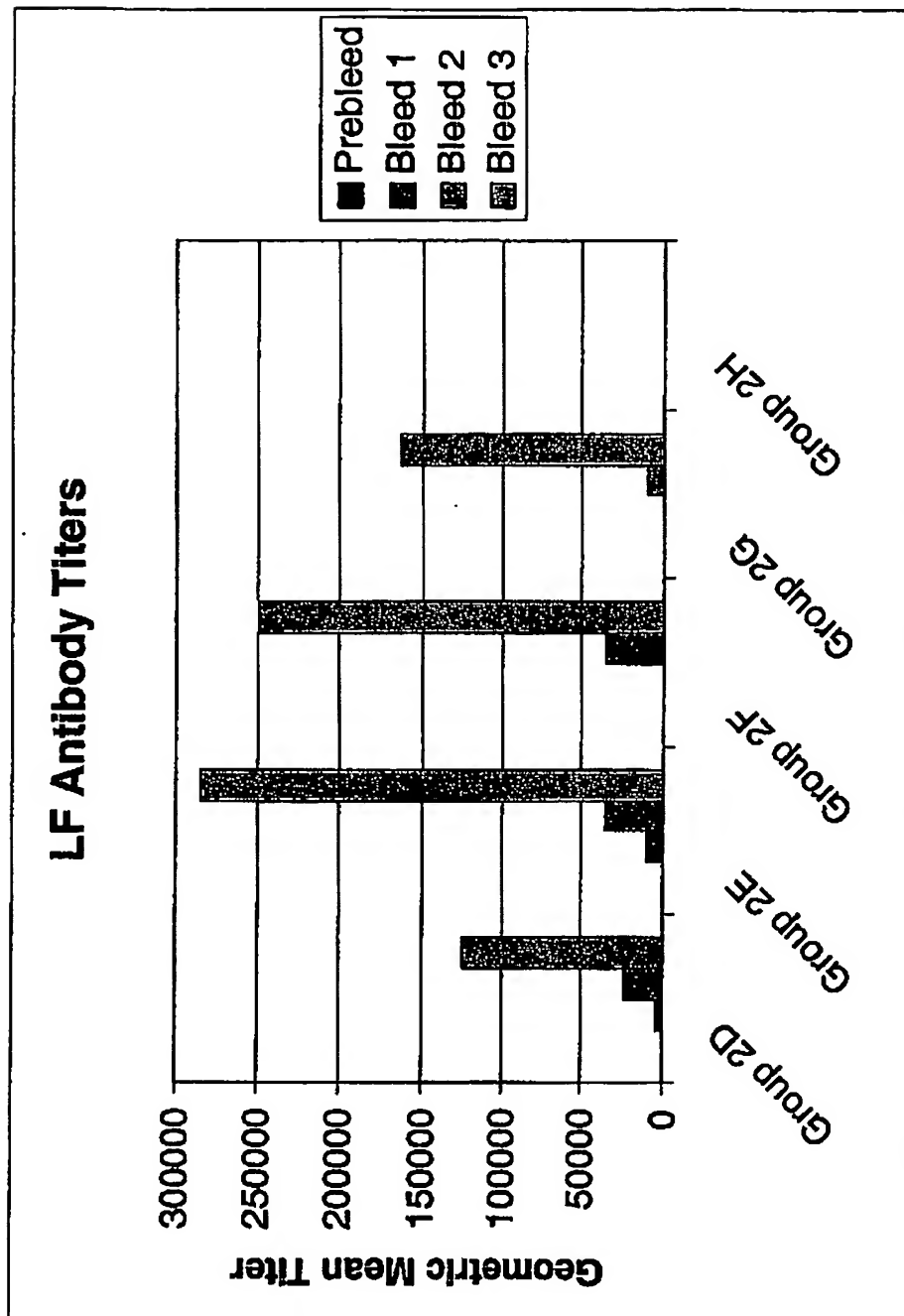


FIG. 16B

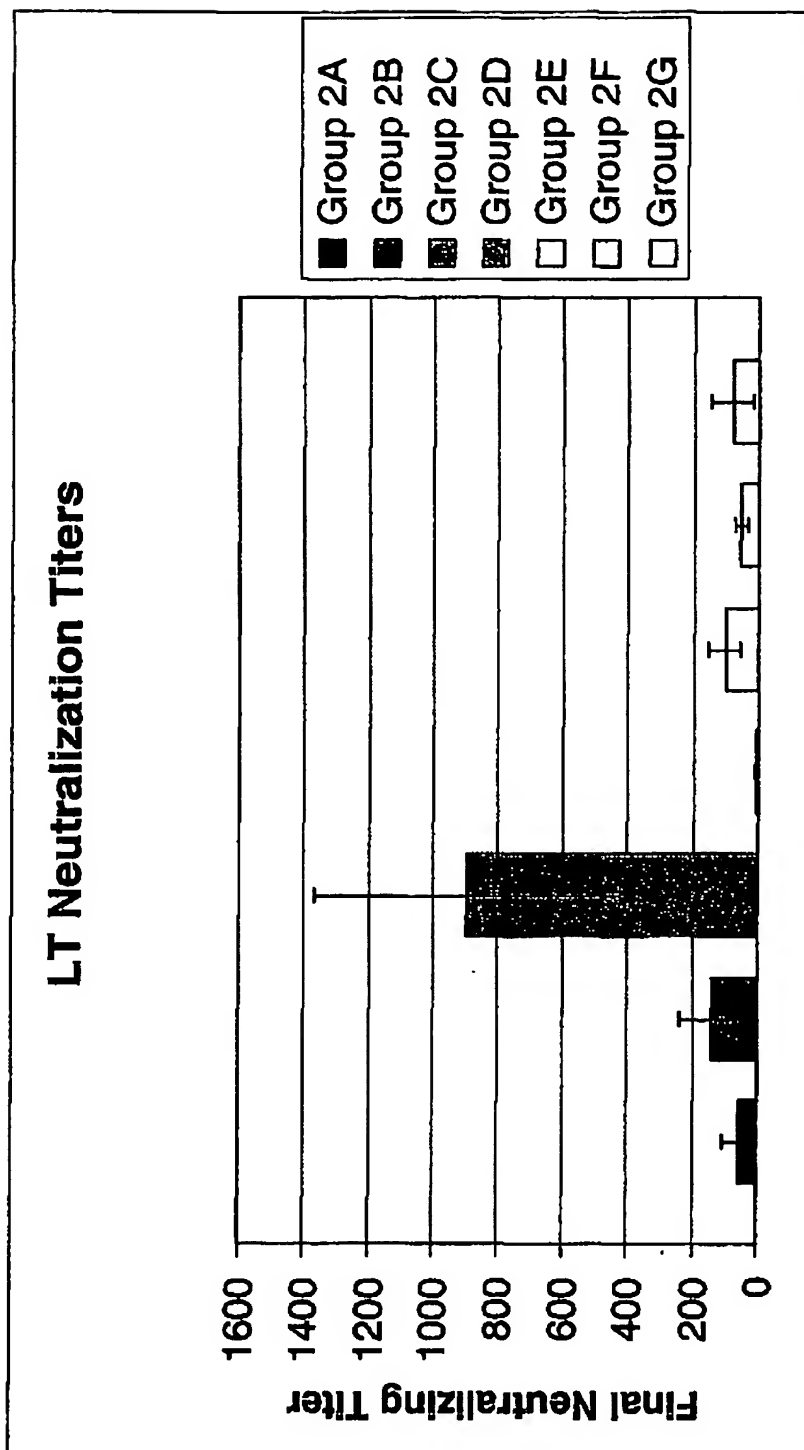


FIG. 16C

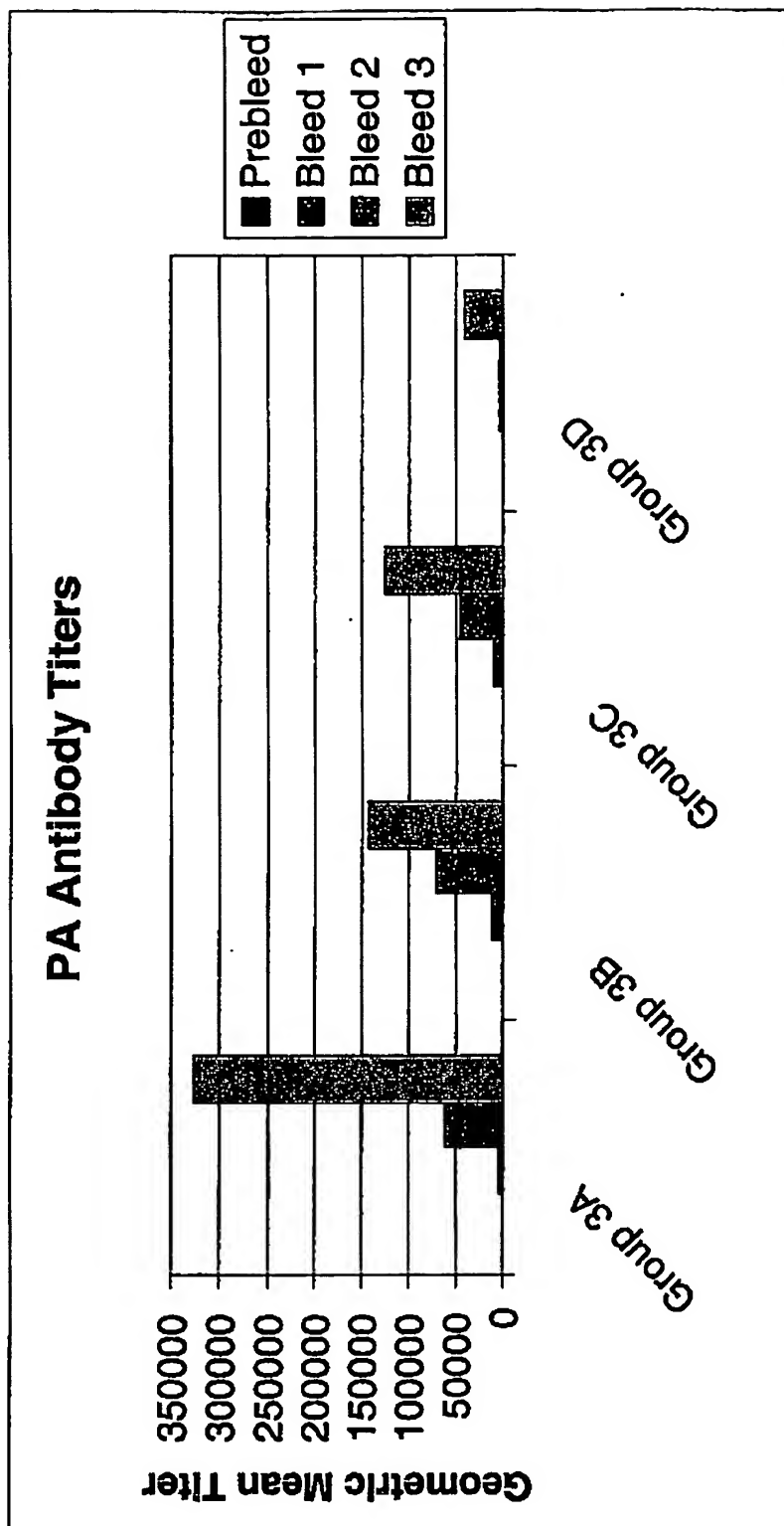


FIG. 17A

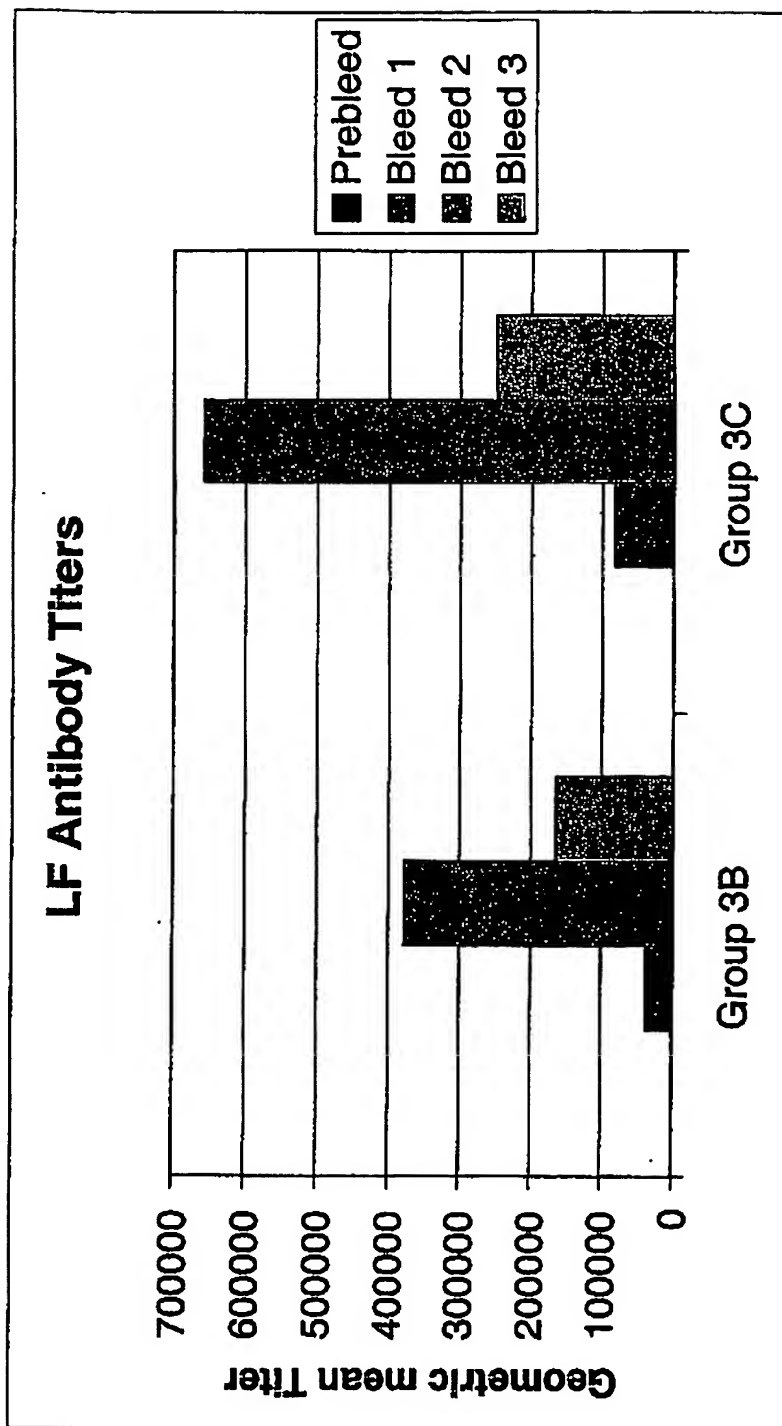


FIG. 17B

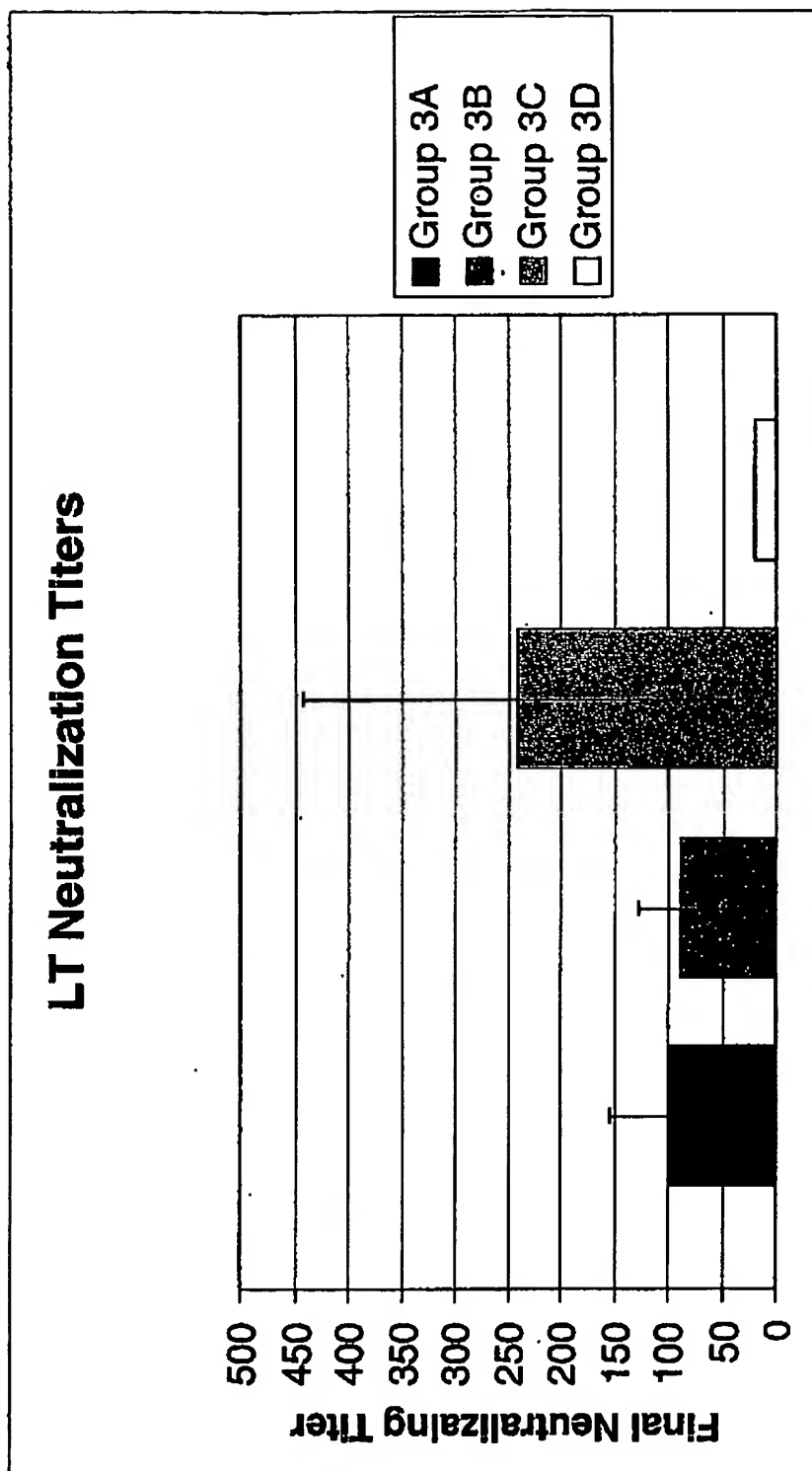


FIG. 17C

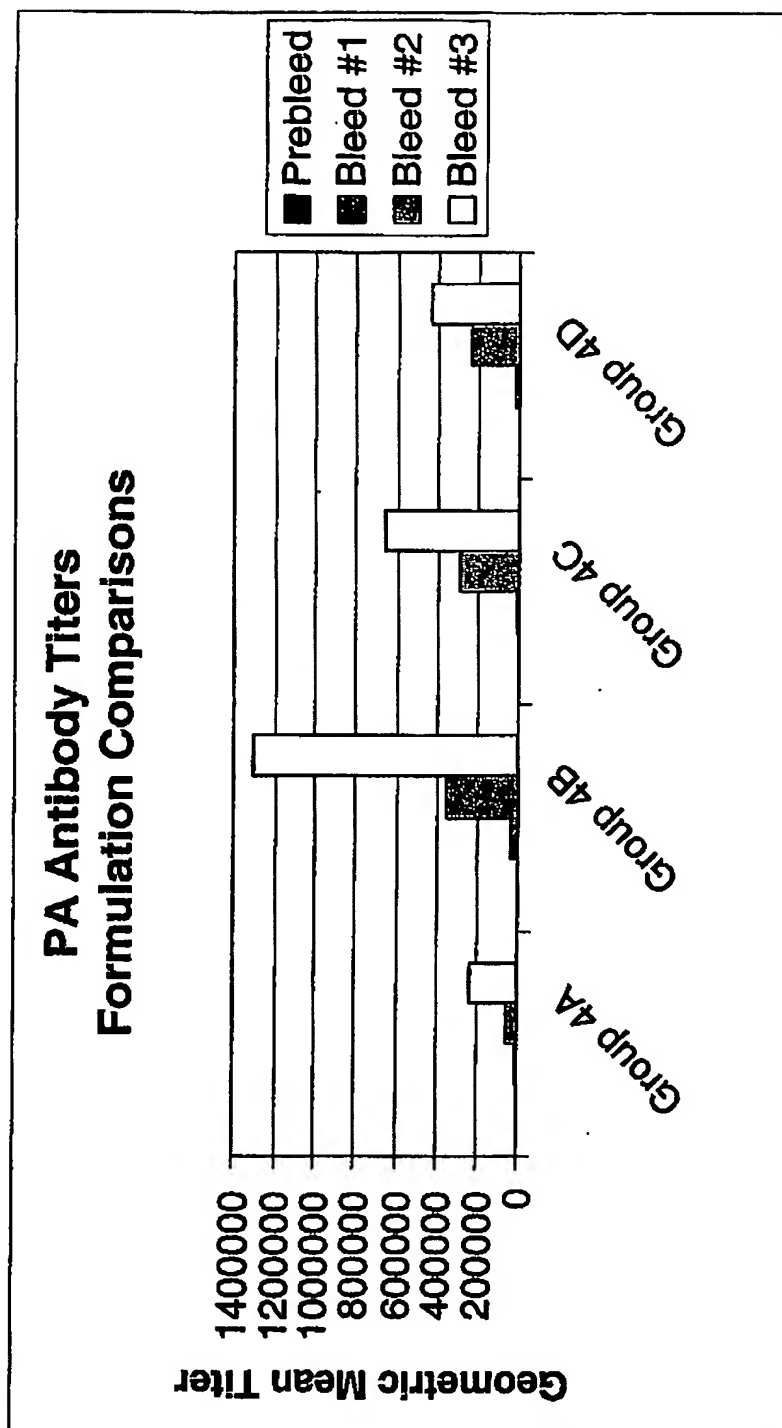
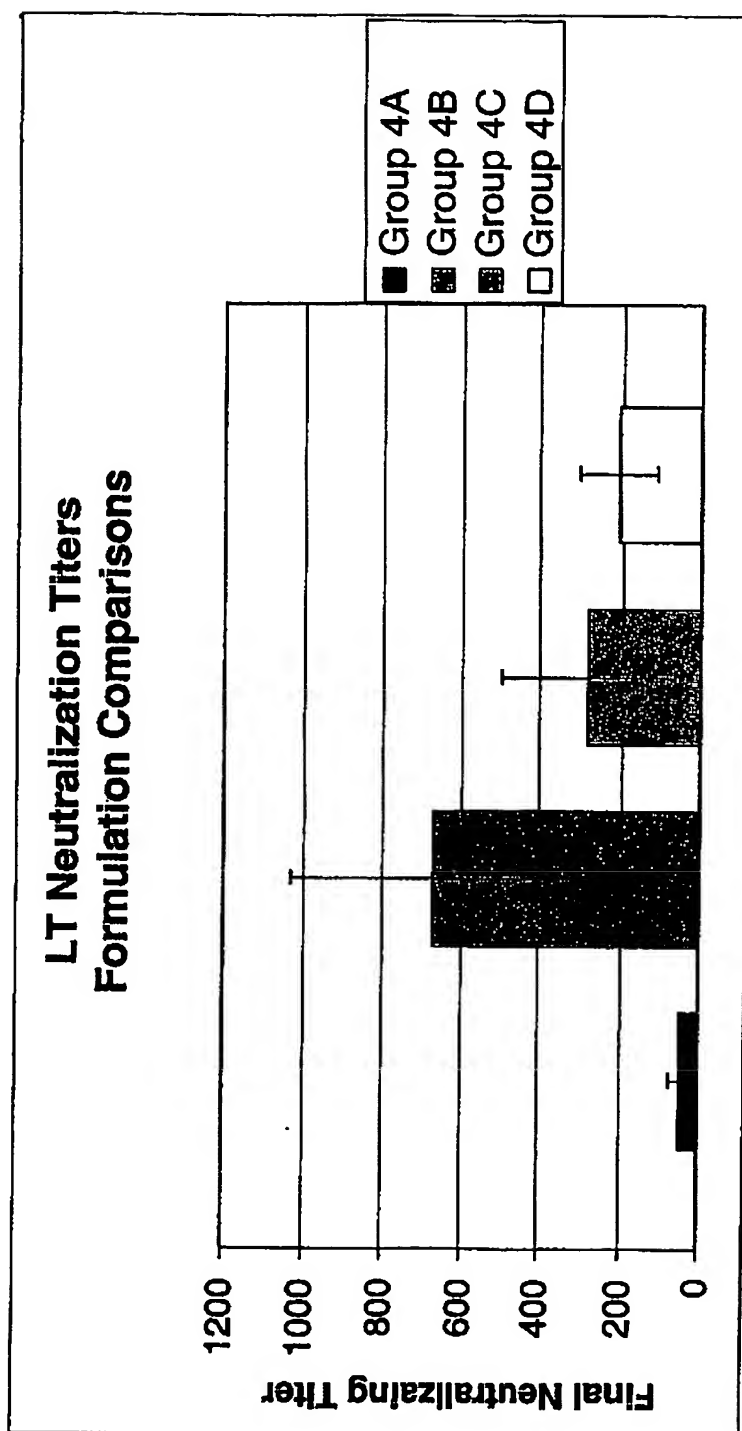


FIG. 18A

**FIG. 18B**

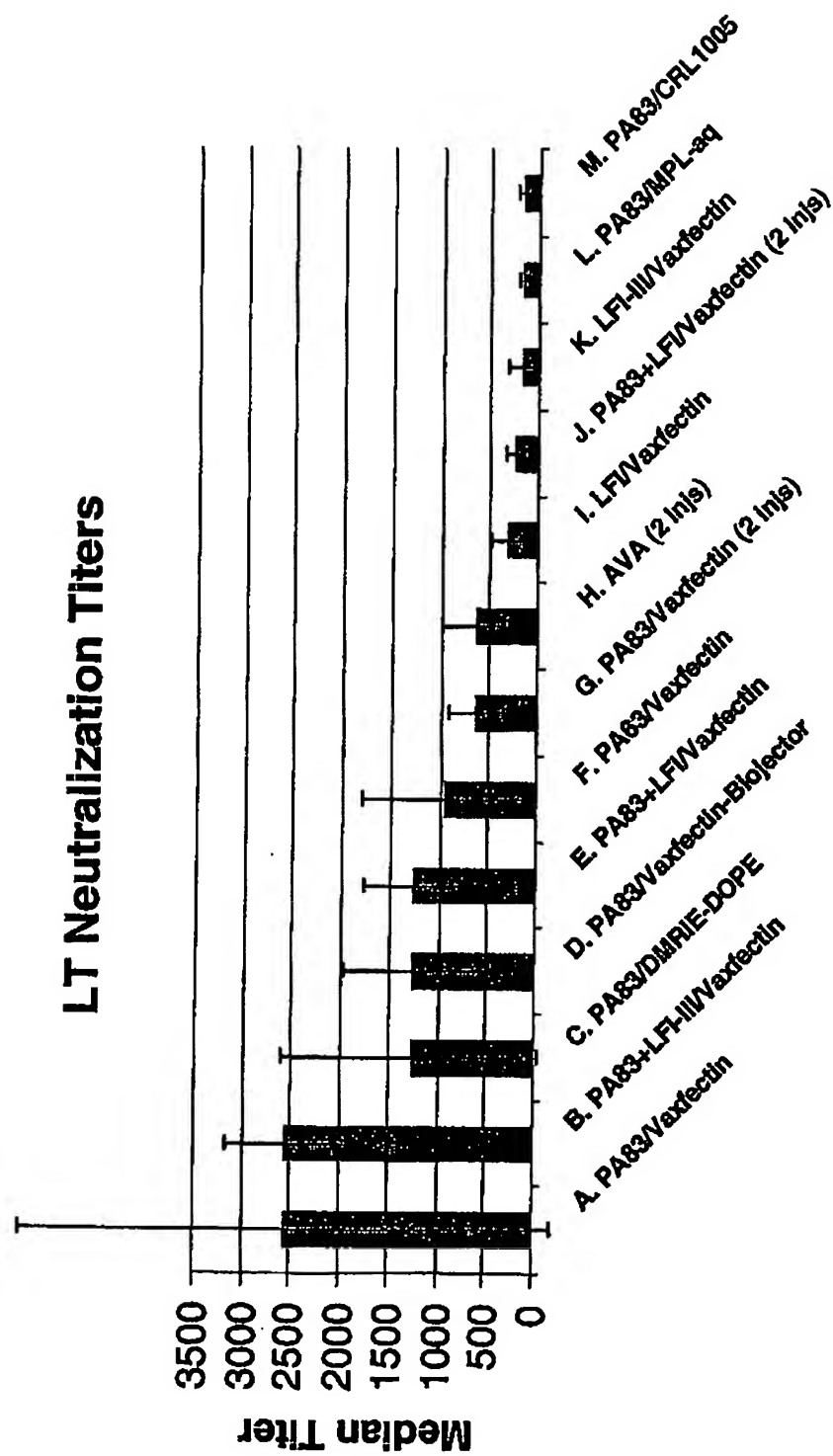


FIG. 19

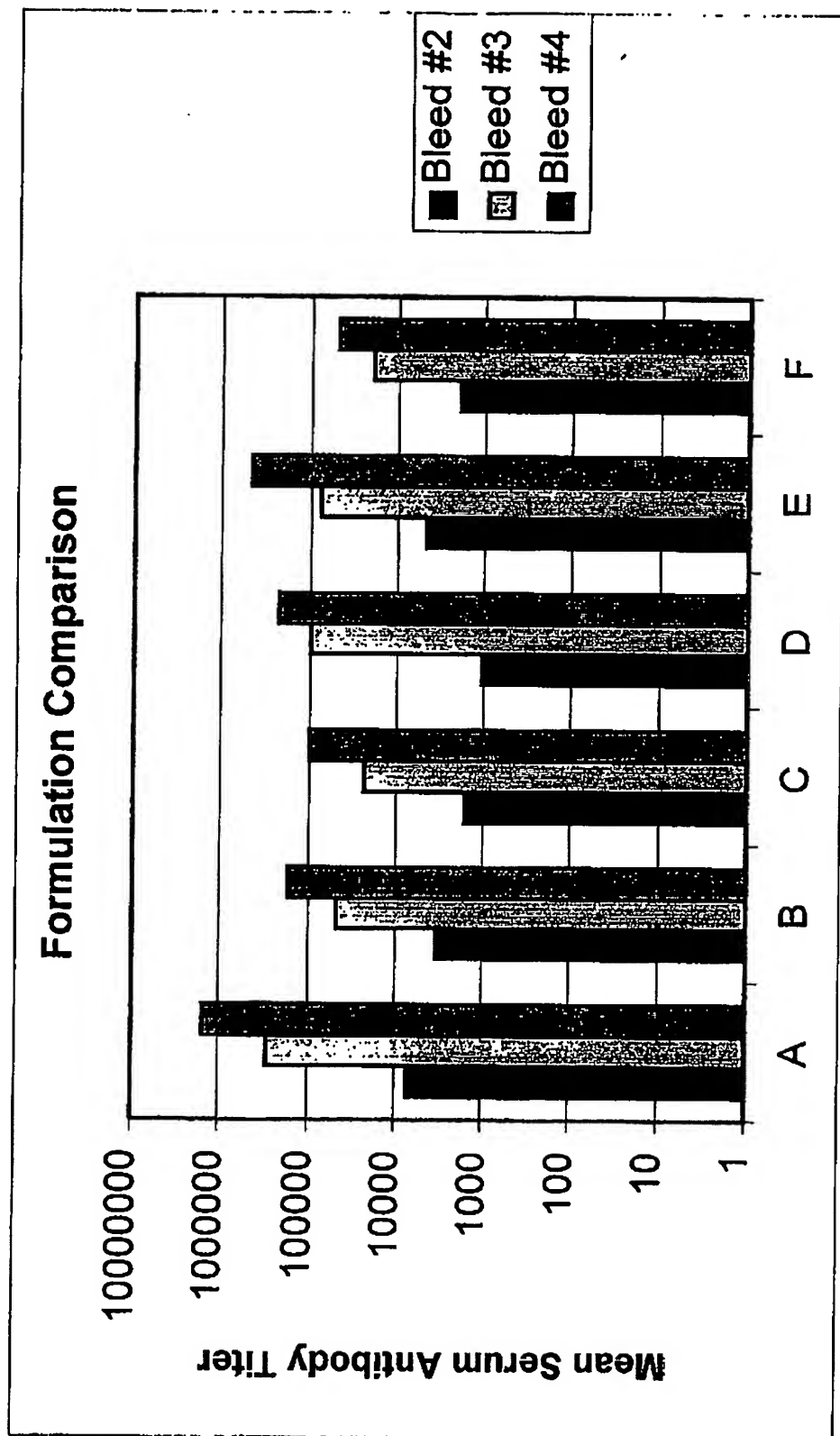


FIGURE 20

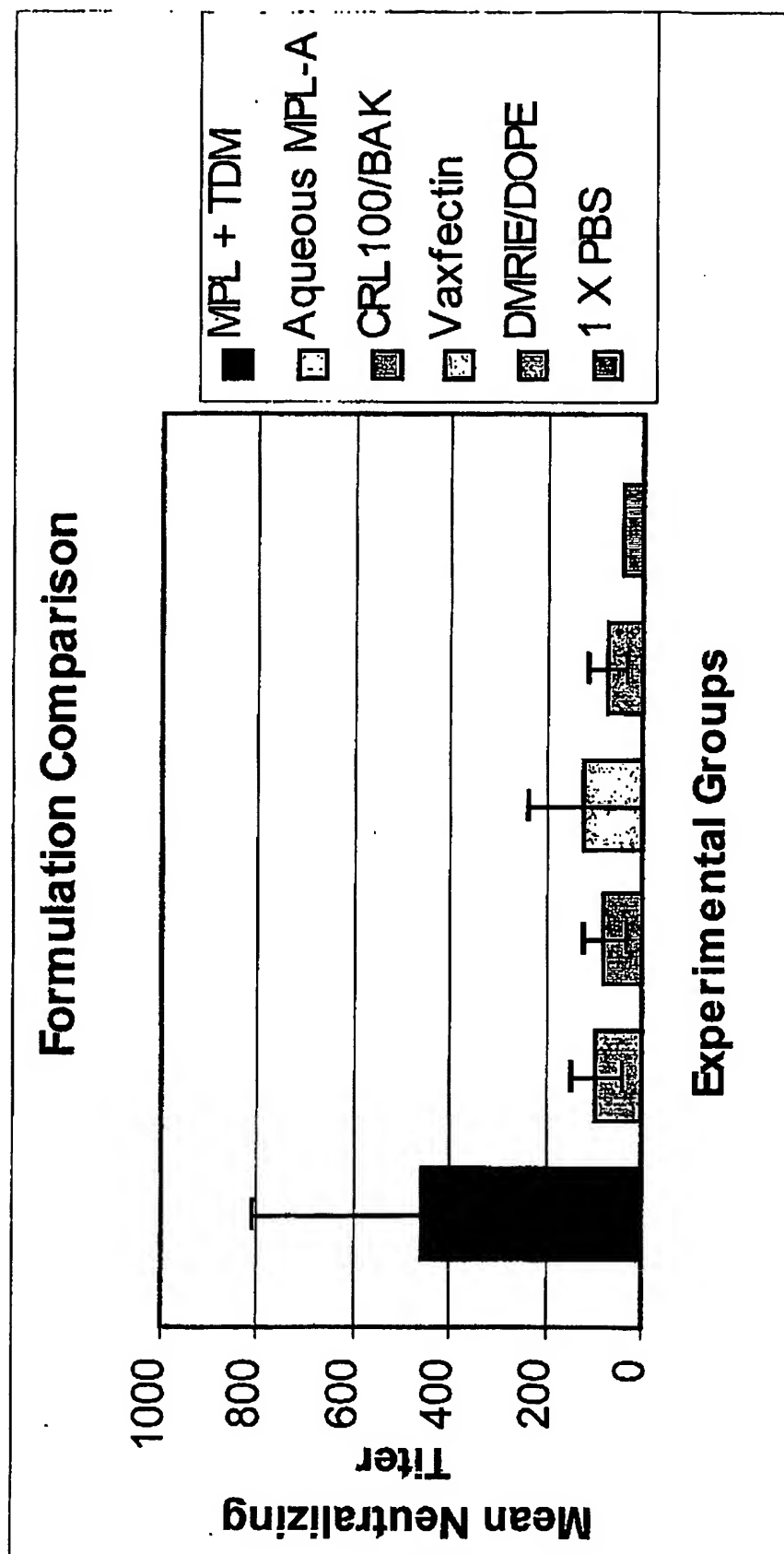


FIGURE 21

-1-

SEQUENCE LISTING

<110> Vical Incorporated

<120> Codon-Optimized Polynucleotide-Based Vaccines
Against Bacillus anthracis Infection

<130> 1530.046PC03

<150> US 60/409,307

<151> 2002-09-10

<150> US 60/419,089

<151> 2002-10-18

<160> 76

<170> PatentIn version 3.1

<210> 1

<211> 1788

<212> DNA

<213> Artificial Sequence

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<223> Synthetic coding region for Human TPA/B. anthracis
antigen fusion protein

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<221> CDS

<222> (13)..(1779)

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ctg tgt gga gca gtc ttc gtt tgc ccc agc agc gct ggg cca act gtg 99

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Leu	Cys	Gly	Ala	Val	Phe	Val	Ser	Pro	Ser	Ser	Ala	Gly	Pro	Thr	Val		
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ccc	gac	aga	gac	aat	gat	gga	atc	cct	gat	agt	cta	gag	gtt	gag	gga	147	
Pro	Asp	Arg	Asp	Asn	Asp	Gly	Ile	Pro	Asp	Ser	Leu	Glu	Val	Glu	Gly		
30				35					40					45			
tac	acg	gta	gat	gtc	aag	aac	aaa	agg	act	ttt	ctc	tcg	cct	tgg	atc	195	
Tyr	Thr	Val	Asp	Val	Lys	Asn	Lys	Arg	Thr	Phe	Leu	Ser	Pro	Trp	Ile		
				50				55					60				
tca	aat	atc	cat	gag	aag	aag	ggg	ctt	acc	aag	tac	aag	tcc	tcc	ccc	243	
Ser	Asn	Ile	His	Glu	Lys	Lys	Gly	Leu	Thr	Lys	Tyr	Lys	Ser	Ser	Pro		
			65				70					75					
gag	aag	tgg	tct	acc	gct	tcc	gat	cca	tat	agc	gat	ttc	gag	aag	gtc	291	
Glu	Lys	Trp	Ser	Thr	Ala	Ser	Asp	Pro	Tyr	Ser	Asp	Phe	Glu	Lys	Val		
	80					85					90						
aca	ggc	cgg	atc	gat	aaa	aat	gtg	tct	cca	gag	gct	aga	cac	ccc	ctg	339	
Thr	Gly	Arg	Ile	Asp	Lys	Asn	Val	Ser	Pro	Glu	Ala	Arg	His	Pro	Leu		
	95				100					105							
gta	gca	gcc	tac	ccg	att	gta	cac	gtg	gac	atg	gag	aac	atc	att	cta	387	
Val	Ala	Ala	Tyr	Pro	Ile	Val	His	Val	Asp	Met	Glu	Asn	Ile	Ile	Leu		
110				115				120						125			
agc	aaa	aac	gag	gac	cag	tcc	aca	caa	aac	act	gac	tcc	gag	acc	cgc	435	
Ser	Lys	Asn	Glu	Asp	Gln	Ser	Thr	Gln	Asn	Thr	Asp	Ser	Glu	Thr	Arg		
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acc	ata	tct	aaa	aac	acc	agt	act	tca	agg	acc	cac	acc	tct	gaa	gtg	483	
Thr	Ile	Ser	Lys	Asn	Thr	Ser	Thr	Ser	Arg	Thr	His	Thr	Ser	Glu	Val		
			145			150						155					
cac	ggc	aat	gcg	gaa	gtc	cat	gca	tcg	ttt	ttc	gat	att	ggg	ggc	tcc	531	
His	Gly	Asn	Ala	Glu	Val	His	Ala	Ser	Phe	Phe	Asp	Ile	Gly	Gly	Ser		
		160				165					170						
gtg	tca	gcc	ggc	ttt	agc	aat	agc	aac	tcc	tcg	acg	gtt	gcc	att	gac	579	
Val	Ser	Ala	Gly	Phe	Ser	Asn	Ser	Asn	Ser	Ser	Thr	Val	Ala	Ile	Asp		
	175				180				185								
cac	tca	ctg	tca	tta	gca	ggg	gag	agg	act	tgg	gct	gaa	act	atg	ggg	627	
His	Ser	Leu	Ser	Leu	Ala	Gly	Glu	Arg	Thr	Trp	Ala	Glu	Thr	Met	Gly		
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Leu	Asn	Thr	Ala	Asp	Thr	Ala	Arg	Leu	Asn	Ala	Asn	Ile	Arg	Tyr	Val		
			210				215					220					
aac	aca	ggg	act	gct	cct	ata	tat	aac	gtg	ctg	cct	acg	aca	agt	ctt	723	
Asn	Thr	Gly	Thr	Ala	Pro	Ile	Tyr	Asn	Val	Leu	Pro	Thr	Thr	Ser	Leu		
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gtc	ctg	ggc	aaa	aat	cag	acc	ctc	gca	acc	att	aag	gca	aag	gaa	aat	771	
Val	Leu	Gly	Lys	Asn	Gln	Thr	Leu	Ala	Thr	Ile	Lys	Ala	Lys	Glu	Asn		
	240				245			250									
cag	ctg	agc	cag	atc	ctc	gcc	cct	aac	aac	tat	tat	cca	tcc	aaa	aat	819	
Gln	Leu	Ser	Gln	Ile	Leu	Ala	Pro	Asn	Asn	Tyr	Tyr	Pro	Ser	Lys	Asn		
	255				260					265							

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tta gcc ccc ata gcc ctg aac gcc cag gac gac ttt tcc tct acc ccc Leu Ala Pro Ile Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro 270 275 280 285	867
ata act atg aat tac aat cag ttc ctg gag ctg gaa aag acg aag cag Ile Thr Met Asn Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln 290 295 300	915
ctg aga cta gac acc gat cag gtg tat gga aac ata gcg aca tat aac Leu Arg Leu Asp Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn 305 310 315	963
ttt gag aac ggc cgc gtg cgc gtc gac act ggg tca aac tgg tct gaa Phe Glu Asn Gly Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu 320 325 330	1011
gtt ctg ccg caa att caa gag aca acc gcc aga att atc ttt aat ggg Val Leu Pro Gln Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly 335 340 345	1059
aag gac ttg aac ctt gtc gaa cgt aga att gcc gcc gtg aac ccc agt Lys Asp Leu Asn Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser 350 355 360 365	1107
gat cca ctc gag acg act aaa ccg gat atg aca ctg aaa gag gct ctg Asp Pro Leu Glu Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu 370 375 380	1155
aag att gcc ttc gga ttc aac gaa cct aat ggc aat ttg cag tat cag Lys Ile Ala Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln 385 390 395	1203
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acg gtt ctc gat aaa atc aaa ctt aac gcc aag atg aac ata ttg att Thr Val Leu Asp Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile 430 435 440 445	1347
cga gac aaa cgc ttc cac tac gac cgc aac aat ata gcc gta ggc gct Arg Asp Lys Arg Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala 450 455 460	1395
gat gag tct gtc gtc aag gag gct cat agg gaa gtt atc aac agc agt Asp Glu Ser Val Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser 465 470 475	1443
act gaa ggg ctg tta ctt aat atc gac aag gac att cgg aag atc ctg Thr Glu Gly Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu 480 485 490	1491
tcc ggg tat atc gtg gag atc gag gat acc gag ggc ctg aag gaa gtc Ser Gly Tyr Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val 495 500 505	1539
att aac gac cgc tat gat atg ctg aac att tcc agc tta cga cag gac Ile Asn Asp Arg Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp	1587

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510	515	520	525	
ggt aag aca ttt att gac ttt aaa aag tat aac gac aag cta ccc ctg				1635
Gly Lys Thr Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu	530	535	540	
tac att tcc aac cca aat tac aaa gtt aat gtg tat gct gta acc aag				1683
Tyr Ile Ser Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys	545	550	555	
gag aac aca atc atc aat cca agc gag aac ggc gat acc agc aca aat				1731
Glu Asn Thr Ile Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn	560	565	570	
gga atc aaa aag atc ctt ata ttt agt aaa aaa ggc tac gag atc ggt				1779
Gly Ile Lys Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly	575	580	585	
tgaggatcc				1788

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<212> PRT

<213> Artificial Sequence

<220>

<223> Human TPA/ B. anthracis antigen fusion protein

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Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val	
35 40 45	

Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile	
50 55 60	

His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp	
65 70 75 80	

Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg	
85 90 95	

Ile Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala	
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-5-

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Tyr Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn 115 120 125		
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Lys Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn 145 150 155 160		
Ala Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala 165 170 175		
Gly Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu 180 185 190		
Ser Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr 195 200 205		
Ala Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly 210 215 220		
Thr Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly 225 230 235 240		
Lys Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser 245 250 255		
Gln Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro 260 265 270		
Ile Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met 275 280 285		
Asn Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu 290 295 300		
Asp Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn 305 310 315 320		
Gly Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro 325 330 335		
Gln Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu 340 345 350		

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Asn Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu
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Glu Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala
 370 375 380

Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp
 385 390 395 400

Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile
 405 410 415

Lys Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu
 420 425 430

Asp Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys
 435 440 445

Arg Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser
 450 455 460

Val Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly
 465 470 475 480

Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr
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Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp
 500 505 510

Arg Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr
 515 520 525

Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser
 530 535 540

Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr
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Ile Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys
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Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
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<210> 3

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<211> 4235

<212> DNA

<213> *Bacillus anthracis*

<220>

<221> CDS

<222> (1804) .. (4098)

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aaaagacagt tgatgctatt actccagata aaatatagct aaccataaat ttattaaga 180
aaccttggtg ttctaaataa tgattttgtg gattccggaa tagatactgg tgagttagct 240
ctaattttat agtgatttaa ctaacaattt ataaagcagc ataattcaaa ttttttaatt 300
gatttttcct gaagcatagt ataaaagagt caaggctctc tagacttgac tcttggaatc 360
attaggaatt aacaatatat ataatgcgct agacagaatc aaattaaatg caaaaatgaa 420
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ccagttcttt	tatccgaact	gatacacgta	tttttagcata	atttttaatg	tatcttcaaa	1620		
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tat atg aaa	aaa cga	aaa gtg	tta ata	cca tta	atg gca	ttg tct acg	1848	
Met Lys Lys	Arg Lys	Val Leu	Ile Pro	Leu Met	Ala Leu	Ser Thr		
1		5		10		15		
ata tta gtt	tca agc	aca ggt	aat tta	gag gtg	att cag	gca gaa	gtt	1896
Ile Leu Val	Ser Ser	Thr Gly	Asn Leu	Glu Val	Ile Gln	Ala Glu	Val	
	20			25		30		
aaa cag gag	aac cgg	tta tta	aat gaa	tca gaa	tca agt	tcc cag	ggg	1944
Lys Gln Glu	Asn Arg	Leu Leu	Asn Glu	Ser Glu	Ser Ser	Ser Gln	Gly	
	35		40			45		
tta cta gga	tac tat	ttt agt	gat ttg	aat ttt	caa gca	ccc atg	gtg	1992
Leu Leu Gly	Tyr Tyr	Phe Ser	Asp Leu	Asn Phe	Gln Ala	Pro Met	Val	
	50		55		60			
gtt acc tct	tct act	aca ggg	gat tta	tct att	cct agt	tct gag	tta	2040
Val Thr Ser	Ser Thr	Thr Gly	Asp Leu	Ser Ile	Pro Ser	Ser Ser	Glu Leu	
65		70		75				
gaa aat att	cca tcg	gaa aac	caa tat	ttt caa	tct gct	att tgg	tca	2088
Glu Asn Ile	Pro Ser	Glu Asn	Gln Tyr	Phe Gln	Ser Ala	Ile Trp	Ser	
80		85		90		95		
gga ttt atc	aaa gtt	aag aag	agt gat	gaa tat	aca ttt	gct act	tcc	2136
Gly Phe Ile	Lys Val	Lys Lys	Ser Asp	Glu Tyr	Thr Phe	Ala Thr	Ser	
	100		105			110		
gct gat aat	cat gta	aca atg	tgg gta	gat gac	caa gaa	gtg att	aat	2184
Ala Asp Asn	His Val	Thr Met	Trp Val	Asp Asp	Gln Glu	Val Ile	Asn	
	115		120		125			
aaa gct tct	aat tct	aac aaa	atc aga	tta gaa	aaa gga	aga tta	tat	2232
Lys Ala Ser	Asn Ser	Asn Lys	Ile Arg	Leu Glu	Lys Gly	Arg Leu	Tyr	
	130		135		140			
caa ata aaa	att caa	tat caa	cga gaa	aat cct	act gaa	aaa gga	ttg	2280
Gln Ile Lys	Ile Gln	Tyr Gln	Arg Glu	Asn Pro	Thr Glu	Lys Gly	Leu	
	145		150		155			
gat ttc aag	ttg tac	tgg acc	gat tct	caa aat	aaa aaa	gaa gtg	att	2328
Asp Phe Lys	Leu Tyr	Trp Thr	Asp Ser	Gln Asn	Lys Lys	Glu Val	Ile	
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tct agt gat	aac tta	caa ttg	cca gaa	tta aaa	caa aaa	tct tcg	aac	2376
Ser Ser Asp	Asn Leu	Gln Leu	Pro Glu	Leu Lys	Gln Lys	Ser Ser	Asn	

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180										185										190									
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Ser	Arg	Lys	Lys	Arg	Ser	Thr	Ser	Ala	Gly	Pro	Thr	Val	Pro	Asp	Arg														
			195					200					205																
gac	aat	gat	gga	atc	cct	gat	tca	tta	gag	gta	gaa	gga	tat	acg	gtt					2472									
Asp	Asn	Asp	Gly	Ile	Pro	Asp	Ser	Leu	Glu	Val	Glu	Gly	Tyr	Thr	Val														
		210					215					220																	
gat	gtc	aaa	aat	aaa	aga	act	ttt	ctt	tca	cca	tgg	att	tct	aat	att					2520									
Asp	Val	Lys	Asn	Lys	Arg	Thr	Phe	Leu	Ser	Pro	Trp	Ile	Ser	Asn	Ile														
	225					230					235																		
cat	gaa	aag	aaa	gga	tta	acc	aaa	tat	aaa	tca	tct	cct	gaa	aaa	tgg					2568									
His	Glu	Lys	Lys	Gly	Leu	Thr	Lys	Tyr	Lys	Ser	Ser	Pro	Glu	Lys	Trp														
240					245					250					255														
agc	acg	gct	tct	gat	ccg	tac	agt	gat	ttc	gaa	aag	gtt	aca	gga	cgg					2616									
Ser	Thr	Ala	Ser	Asp	Pro	Tyr	Ser	Asp	Phe	Glu	Lys	Val	Thr	Gly	Arg														
				260				265						270															
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Ile	Asp	Lys	Asn	Val	Ser	Pro	Glu	Ala	Arg	His	Pro	Leu	Val	Ala	Ala														
		275					280					285																	
tat	ccg	att	gta	cat	gta	gat	atg	gag	aat	att	att	ctc	tca	aaa	aat					2712									
Tyr	Pro	Ile	Val	His	Val	Asp	Met	Glu	Asn	Ile	Ile	Leu	Ser	Lys	Asn														
	290					295						300																	
gag	gat	caa	tcc	aca	cag	aat	act	gat	agt	gaa	acg	aga	aca	ata	agt					2760									
Glu	Asp	Gln	Ser	Thr	Gln	Asn	Thr	Asp	Ser	Glu	Thr	Arg	Thr	Ile	Ser														
	305					310					315																		
aaa	aat	act	tct	aca	agt	agg	aca	cat	act	agt	gaa	gta	cat	gga	aat					2808									
Lys	Asn	Thr	Ser	Thr	Ser	Arg	Thr	His	Thr	Ser	Glu	Val	His	Gly	Asn														
320					325					330				335															
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Ala	Glu	Val	His	Ala	Ser	Phe	Phe	Asp	Ile	Gly	Gly	Ser	Val	Ser	Ala														
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Gly	Phe	Ser	Asn	Ser	Asn	Ser	Ser	Thr	Val	Ala	Ile	Asp	His	Ser	Leu														
		355					360					365																	
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Ser	Leu	Ala	Gly	Glu	Arg	Thr	Trp	Ala	Glu	Thr	Met	Gly	Leu	Asn	Thr														
	370					375					380																		
gct	gat	aca	gca	aga	tta	aat	gcc	aat	att	aga	tat	gta	aat	act	ggg					3000									
Ala	Asp	Thr	Ala	Arg	Leu	Asn	Ala	Asn	Ile	Arg	Tyr	Val	Asn	Thr	Gly														
	385				390					395																			
acg	gct	cca	atc	tac	aac	gtg	tta	cca	acg	act	tcg	tta	gtg	tta	gga					3048									
Thr	Ala	Pro	Ile	Tyr	Asn	Val	Leu	Pro	Thr	Thr	Ser	Leu	Val	Leu	Gly														
400					405				410					415															
aaa	aat	caa	aca	ctc	gcg	aca	att	aaa	gct	aag	gaa	aac	caa	tta	agt					3096									
Lys	Asn	Gln	Thr	Leu	Ala	Thr	Ile	Lys	Ala	Lys	Glu	Asn	Gln	Leu	Ser														
			420					425					430																

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Gln Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro	
435 440 445	
atc gca tta aat gca caa gac gat ttc agt tct act cca att aca atg	3192
Ile Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met	
450 455 460	
aat tac aat caa ttt ctt gag tta gaa aaa acg aaa caa tta aga tta	3240
Asn Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu	
465 470 475	
gat acg gat caa gta tat ggg aat ata gca aca tac aat ttt gaa aat	3288
Asp Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn	
480 485 490 495	
gga aga gtg agg gtg gat aca ggc tcg aac tgg agt gaa gtg tta ccg	3336
Gly Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro	
500 505 510	
caa att caa gaa aca act gca cgt atc att ttt aat gga aaa gat tta	3384
Gln Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu	
515 520 525	
aat ctg gta gaa agg cgg ata gcg gcg gtt aat cct agt gat cca tta	3432
Asn Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu	
530 535 540	
gaa acg act aaa ccg gat atg aca tta aaa gaa gcc ctt aaa ata gca	3480
Glu Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala	
545 550 555	
ttt gga ttt aac gaa ccg aat gga aac tta caa tat caa ggg aaa gac	3528
Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp	
560 565 570 575	
ata acc gaa ttt gat ttt aat ttc gat caa caa aca tct caa aat atc	3576
Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile	
580 585 590	
aag aat cag tta gcg gaa tta aac gca act aac ata tat act gta tta	3624
Lys Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu	
595 600 605	
gat aaa atc aaa tta aat gca aaa atg aat att tta ata aga gat aaa	3672
Asp Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys	
610 615 620	
cgt ttt cat tat gat aga aat aac ata gca gtt ggg gcg gat gag tca	3720
Arg Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser	
625 630 635	
gta gtt aag gag gct cat aga gaa gta att aat tcg tca aca gag gga	3768
Val Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly	
640 645 650 655	
tta ttg tta aat att gat aag gat ata aga aaa ata tta tca ggt tat	3816
Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr	
660 665 670	
att gta gaa att gaa gat act gaa ggg ctt aaa gaa gtt ata aat gac	3864
Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp	

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675	680	685	
aga tat gat atg ttg aat att tct agt tta cgg caa gat gga aaa aca			3912
Arg Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr			
690	695	700	
ttt ata gat ttt aaa aaa tat aat gat aaa tta ccg tta tat ata agt			3960
Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser			
705	710	715	
aat ccc aat tat aag gta aat gta tat gct gtt act aaa gaa aac act			4008
Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr			
720	725	730	735
att att aat cct agt gag aat ggg gat act agt acc aac ggg atc aag			4056
Ile Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys			
740	745	750	
aaa att tta atc ttt tct aaa aaa ggc tat gag ata gga taa			4098
Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly			
755	760		
ggtaattcta ggtgattttt aaattatcta aaaaacagta aaattaaaac atactctttt			4158
tgtaagaaat acaaggagag tatgttttaa acagtaatct aaatcatcat aatcctttga			4218
gattgtttgt aggatcc			4235
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Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys			
20	25	30	
Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu			
35	40	45	
Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val			
50	55	60	
Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu			
65	70	75	80
Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly			

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85	90	95
Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala 100 105 110		
Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys 115 120 125		
Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln 130 135 140		
Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp 145 150 155 160		
Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser 165 170 175		
Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser 180 185 190		
Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp 195 200 205		
Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp 210 215 220		
Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His 225 230 235 240		
Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser 245 250 255		
Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile 260 265 270		
Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr 275 280 285		
Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu 290 295 300		
Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg Thr Ile Ser Lys 305 310 315 320		
Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala 325 330 335		

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Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly
 340 345 350

Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser
 355 360 365

Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala
 370 375 380

Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr
 385 390 395 400

Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys
 405 410 415

Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln
 420 425 430

Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile
 435 440 445

Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn
 450 455 460

Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp
 465 470 475 480

Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly
 485 490 495

Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln
 500 505 510

Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn
 515 520 525

Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu
 530 535 540

Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe
 545 550 555 560

Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile
 565 570 575

Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys
 580 585 590

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Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp
 595 600 605

Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg
 610 615 620

Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val
 625 630 635 640

Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu
 645 650 655

Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile
 660 665 670

Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg
 675 680 685

Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe
 690 695 700

Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn
 705 710 715 720

Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile
 725 730 735

Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys
 740 745 750

Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
 755 760

<210> 5

<211> 1782

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region for Human TPA/synthetic
 antigen fusion protein

<220>

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<221> CDS

<222> (13)..(1773)

<223>

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1 5 10	
ctg tgt gga gca gtc ttc gtt tcg ccc agc agc gct ggg cca act gtg	99
Leu Cys Gly Ala Val Phe Val Ser Pro Ser Ser Ala Gly Pro Thr Val	
15 20 25	
ccc gac aga gac aat gat gga atc cct gat agt cta gag gtt gag gga	147
Pro Asp Arg Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly	
30 35 40 45	
tac acg gta gat gtc aag aac aaa agg act ttt ctc tcg cct tgg atc	195
Tyr Thr Val Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile	
50 55 60	
tca aat atc cat gag aag aag ggg ctt acc aag tac aag tcc tcc ccc	243
Ser Asn Ile His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro	
65 70 75	
gag aag tgg tct acc gct tcc gat cca tat agc gat ttc gag aag gtc	291
Glu Lys Trp Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val	
80 85 90	
aca ggc cgg atc gat aaa aat gtg tct cca gag gct aga cac ccc ctg	339
Thr Gly Arg Ile Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu	
95 100 105	
gta gca gcc tac ccg att gta cac gtg gac atg gag aac atc att cta	387
Val Ala Ala Tyr Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu	
110 115 120 125	
agc aaa aac gag gac cag tcc aca caa aac act gac tcc gag acc cgc	435
Ser Lys Asn Glu Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg	
130 135 140	
acc ata tct aaa aac acc agt act tca agg acc cac acc tct gaa gtg	483
Thr Ile Ser Lys Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val	
145 150 155	
cac ggc aat gcg gaa gtc cat gca tcg gat att ggt ggc tcc gtg tca	531
His Gly Asn Ala Glu Val His Ala Ser Asp Ile Gly Gly Ser Val Ser	
160 165 170	
gcc ggc ttt agc aat agc aac tcc tcg acg gtt gcc att gac cac tca	579
Ala Gly Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser	
175 180 185	
ctg tca tta gca ggt gag agg act tgg gct gaa act atg ggt ctg aat	627
Leu Ser Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn	
190 195 200 205	
acc gcc gat acg gcc cgg ctc aac gca aat att cgg tac gtc aac aca	675

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Thr	Ala	Asp	Thr	Ala	Arg	Leu	Asn	Ala	Asn	Ile	Arg	Tyr	Val	Asn	Thr	
				210					215					220		
ggg	act	gct	cct	ata	tat	aac	gtg	ctg	cct	acg	aca	agt	ctt	gtc	ctg	723
Gly	Thr	Ala	Pro	Ile	Tyr	Asn	Val	Leu	Pro	Thr	Thr	Ser	Leu	Val	Leu	
			225					230					235			
ggc	aaa	aat	cag	acc	ctc	gca	acc	att	aag	gca	aag	gaa	aat	cag	ctg	771
Gly	Lys	Asn	Gln	Thr	Leu	Ala	Thr	Ile	Lys	Ala	Lys	Glu	Asn	Gln	Leu	
		240					245					250				
agc	cag	atc	ctc	gcc	cct	aac	aac	tat	tat	cca	tcc	aaa	aat	tta	gcc	819
Ser	Gln	Ile	Leu	Ala	Pro	Asn	Asn	Tyr	Tyr	Pro	Ser	Lys	Asn	Leu	Ala	
	255					260					265					
ccc	ata	gcc	ctg	aac	gcc	cag	gac	gac	ttt	tcc	tct	acc	ccc	ata	act	867
Pro	Ile	Ala	Leu	Asn	Ala	Gln	Asp	Asp	Phe	Ser	Ser	Thr	Pro	Ile	Thr	
270					275				280						285	
atg	aat	tac	aat	cag	ttc	ctg	gag	ctg	gaa	aag	acg	aag	cag	ctg	aga	915
Met	Asn	Tyr	Asn	Gln	Phe	Leu	Glu	Leu	Glu	Lys	Thr	Lys	Gln	Leu	Arg	
			290					295					300			
cta	gac	acc	gat	cag	gtg	tat	gga	aac	ata	gcg	aca	tat	aac	ttt	gag	963
Leu	Asp	Thr	Asp	Gln	Val	Tyr	Gly	Asn	Ile	Ala	Thr	Tyr	Asn	Phe	Glu	
			305					310					315			
aac	ggc	cgc	gtg	cgc	gtc	gac	act	ggg	tca	aac	tgg	tct	gaa	gtt	ctg	1011
Asn	Gly	Arg	Val	Arg	Val	Asp	Thr	Gly	Ser	Asn	Trp	Ser	Glu	Val	Leu	
		320					325					330				
ccg	caa	att	caa	gag	aca	acc	gcc	aga	att	atc	ttt	aat	ggg	aag	gac	1059
Pro	Gln	Ile	Gln	Glu	Thr		Ala	Arg	Ile	Ile	Phe	Asn	Gly	Lys	Asp	
	335					340					345					
ttg	aac	ctt	gtc	gaa	cgt	aga	att	gcc	gcc	gtg	aac	ccc	agt	gat	cca	1107
Leu	Asn	Leu	Val	Glu	Arg	Arg	Ile	Ala	Ala	Val	Asn	Pro	Ser	Asp	Pro	
350					355					360					365	
ctc	gag	acg	act	aaa	ccg	gat	atg	aca	ctg	aaa	gag	gct	ctg	aag	att	1155
Leu	Glu	Thr	Thr	Lys	Pro	Asp	Met	Thr	Leu	Lys	Glu	Ala	Leu	Lys	Ile	
			370					375					380			
gcc	ttc	gga	ttc	aac	gaa	cct	aat	ggc	aat	ttg	cag	tat	cag	ggg	aaa	1203
Ala	Phe	Gly	Phe	Asn	Glu	Pro	Asn	Gly	Asn	Leu	Gln	Tyr	Gln	Gly	Lys	
			385					390					395			
gac	atc	aca	gag	ttt	gat	ttc	aat	ttc	gat	cag	cag	act	tcc	caa	aat	1251
Asp	Ile	Thr	Glu	Phe	Asp	Phe	Asn	Phe	Asp	Gln	Gln	Thr	Ser	Gln	Asn	
		400				405						410				
atc	aaa	aat	cag	ttg	gca	gag	ctg	aat	gcc	acc	aat	atc	tac	acg	gtt	1299
Ile	Lys	Asn	Gln	Leu	Ala	Glu	Leu	Asn	Ala	Thr	Asn	Ile	Tyr	Thr	Val	
	415					420					425					
ctc	gat	aaa	atc	aaa	ctt	aac	gcc	aag	atg	aac	ata	ttg	att	cga	gac	1347
Leu	Asp	Lys	Ile	Lys	Leu	Asn	Ala	Lys	Met	Asn	Ile	Leu	Ile	Arg	Asp	
430					435				440						445	
aaa	cgc	ttc	cac	tac	gac	cgc	aac	aat	ata	gcc	gta	ggc	gct	gat	gag	1395
Lys	Arg	Phe	His	Tyr	Asp	Arg	Asn	Asn	Ile	Ala	Val	Gly	Ala	Asp	Glu	
			450					455						460		

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tct gtc gtc aag gag gct cat agg gaa gtt atc aac agc agt act gaa 1443
 Ser Val Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu
 465 470 475

ggg ctg tta ctt aat atc gac aag gac att cgg aag atc ctg tcc ggg 1491
 Gly Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly
 480 485 490

tat atc gtg gag atc gag gat acc gag ggc ctg aag gaa gtc att aac 1539
 Tyr Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn
 495 500 505

gac cgc tat gat atg ctg aac att tcc agc tta cga cag gac ggt aag 1587
 Asp Arg Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys
 510 515 520 525

aca ttt att gac ttt aaa aag tat aac gac aag cta ccc ctg tac att 1635
 Thr Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile
 530 535 540

tcc aac cca aat tac aaa gtt aat gtg tat gct gta acc aag gag aac 1683
 Ser Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn
 545 550 555

aca atc atc aat cca agc gag aac ggc gat acc agc aca aat gga atc 1731
 Thr Ile Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile
 560 565 570

aaa aag atc ctt ata ttt agt aaa aaa ggc tac gag atc ggt tgaggatcc 1782
 Lys Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
 575 580 585

<210> 6

<211> 587

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TPA/synthetic antigen fusion protein

<400> 6

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
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Ala Val Phe Val Ser Pro Ser Ser Ala Gly Pro Thr Val Pro Asp Arg
 20 25 30

Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val
 35 40 45

Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile

50

60

Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp Thr
290 295 300

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Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly Arg
 305 310 315 320

Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln Ile
 325 330 335

Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn Leu
 340 345 350

Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu Thr
 355 360 365

Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe Gly
 370 375 380

Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile Thr
 385 390 395 400

Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys Asn
 405 410 415

Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp Lys
 420 425 430

Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg Phe
 435 440 445

His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val Val
 450 455 460

Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu Leu
 465 470 475 480

Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile Val
 485 490 495

Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg Tyr
 500 505 510

Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe Ile
 515 520 525

Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn Pro
 530 535 540

Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile Ile
 545 550 555 560

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Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys Ile
 565 570 575

Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
 580 585

<210> 7

<211> 2277

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region for Human TPA/synthetic
 antigen fusion protein

<220>

<221> CDS

<222> (13)..(2268)

<223>

<400> 7

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ctg tgt gga gca gtc ttc gtt tcg ccc agc gaa gtg aag caa gaa aat	99
Leu Cys Gly Ala Val Phe Val Ser Pro Ser Glu Val Lys Gln Glu Asn	
15 20 25	
cga ctt ctg aac gag agc gaa agt tca tca cag ggt ctt ctc gga tac	147
Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu Leu Gly Tyr	
30 35 40 45	
tac ttc agt gac ttg aat ttc caa gca cca atg gtg gtg act agt agc	195
Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val Thr Ser Ser	
50 55 60	
acc acc ggc gat ttg agc att ccc agc tct gag ttg gag aac att ccc	243
Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu Asn Ile Pro	
65 70 75	
agc gaa aat cag tac ttc cag tct gct atc tgg tcc gga ttc att aag	291
Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly Phe Ile Lys	
80 85 90	
gtt aaa aag tcc gac gaa tat aca ttt gct acc tcg gcg gat aac cat	339
Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala Asp Asn His	
95 100 105	

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gtg	aca	atg	tgg	gtg	gac	gac	cag	gaa	gtg	atc	aac	aag	gct	tca	aac	387
Val	Thr	Met	Trp	Val	Asp	Asp	Gln	Glu	Val	Ile	Asn	Lys	Ala	Ser	Asn	
110					115					120					125	
tct	aat	aaa	atc	cgg	ctc	gag	aag	ggg	agg	ctc	tac	cag	atc	aaa	att	435
Ser	Asn	Lys	Ile	Arg	Leu	Glu	Lys	Gly	Arg	Leu	Tyr	Gln	Ile	Lys	Ile	
				130					135					140		
cag	tac	cag	cgg	gaa	aac	cct	aca	gaa	aaa	gga	ctc	gat	ttc	aag	ctg	483
Gln	Tyr	Gln	Arg	Glu	Asn	Pro	Thr	Lys	Lys	Gly	Leu	Asp	Phe	Lys	Leu	
			145					150					155			
tac	tgg	aca	gat	agc	caa	aac	aag	aaa	gaa	gtt	atc	agc	tca	gac	aat	531
Tyr	Trp	Thr	Asp	Ser	Gln	Asn	Lys	Lys	Glu	Val	Ile	Ser	Ser	Asp	Asn	
		160					165					170				
ctg	cag	tta	ccc	gag	ctc	aag	cag	aag	agt	tct	aat	aca	agc	gct	ggg	579
Leu	Gln	Leu	Pro	Glu	Leu	Lys	Gln	Lys	Ser	Ser	Asn	Thr	Ser	Ala	Gly	
	175					180					185					
cca	act	gtg	ccc	gac	aga	gac	aat	gat	gga	atc	cct	gat	agt	cta	gag	627
Pro	Thr	Val	Pro	Asp	Arg	Asp	Asn	Asp	Gly	Ile	Pro	Asp	Ser	Leu	Glu	
190				195						200					205	
gtt	gag	gga	tac	acg	gta	gat	gtc	aag	aac	aaa	agg	act	ttt	ctc	tcg	675
Val	Glu	Gly	Tyr	Thr	Val	Asp	Val	Lys	Asn	Lys	Arg	Thr	Phe	Leu	Ser	
				210					215					220		
cct	tgg	atc	tca	aat	atc	cat	gag	aag	aag	ggg	ctt	acc	aag	tac	aag	723
Pro	Trp	Ile	Ser	Asn	Ile	His	Glu	Lys	Lys	Gly	Leu	Thr	Lys	Tyr	Lys	
			225					230					235			
tcc	tcc	ccc	gag	aag	tgg	tct	acc	gct	tcc	gat	cca	tat	agc	gat	ttc	771
Ser	Ser	Pro	Glu	Lys	Trp	Ser	Thr	Ala	Ser	Asp	Pro	Tyr	Ser	Asp	Phe	
		240					245					250				
gag	aag	gtc	aca	ggc	cgg	atc	gat	aaa	aat	gtg	tct	cca	gag	gct	aga	819
Glu	Lys	Val	Thr	Gly	Arg	Ile	Asp	Lys	Asn	Val	Ser	Pro	Glu	Ala	Arg	
	255					260					265					
cac	ccc	ctg	gta	gca	gcc	tac	ccg	att	gta	cac	gtg	gac	atg	gag	aac	867
His	Pro	Leu	Val	Ala	Ala	Tyr	Pro	Ile	Val	His	Val	Asp	Met	Glu	Asn	
270					275					280					285	
atc	att	cta	agc	aaa	aac	gag	gac	cag	tcc	aca	caa	aac	act	gac	tcc	915
Ile	Ile	Leu	Ser	Lys	Asn	Glu	Asp	Gln	Ser	Thr	Gln	Asn	Thr	Asp	Ser	
				290					295					300		
gag	acc	cgc	acc	ata	tct	aaa	aac	acc	agt	act	tca	agg	acc	cac	acc	963
Glu	Thr	Arg	Thr	Ile	Ser	Lys	Asn	Thr	Ser	Thr	Ser	Arg	Thr	His	Thr	
			305					310					315			
tct	gaa	gtg	cac	ggc	aat	gcg	gaa	gtc	cat	gca	tcg	ttt	ttc	gat	att	1011
Ser	Glu	Val	His	Gly	Asn	Ala	Glu	Val	His	Ala	Ser	Phe	Phe	Asp	Ile	
		320					325					330				
ggc	ggc	tcc	gtg	tca	gcc	ggc	ttt	agc	aat	agc	aac	tcc	tcg	acg	gtt	1059
Gly	Gly	Ser	Val	Ser	Ala	Gly	Phe	Ser	Asn	Ser	Asn	Ser	Ser	Thr	Val	
	335					340					345					
gcc	att	gac	cac	tca	ctg	tca	tta	gca	ggc	gag	agg	act	tgg	gct	gaa	1107
Ala	Ile	Asp	His	Ser	Leu	Ser	Leu	Ala	Gly	Glu	Arg	Thr	Trp	Ala	Glu	

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350	355	360	365	
act atg ggt ctg aat acc gcc gat acg gcc cgg ctc aac gca aat att				1155
Thr Met Gly Leu Asn Thr Ala Asp Thr Ala Arg Leu Asn Ala Asn Ile	370	375	380	
cgg tac gtc aac aca ggg act gct cct ata tat aac gtg ctg cct acg				1203
Arg Tyr Val Asn Thr Gly Thr Ala Pro Ile Tyr Asn Val Leu Pro Thr	385	390	395	
aca agt ctt gtc ctg ggc aaa aat cag acc ctc gca acc att aag gca				1251
Thr Ser Leu Val Leu Gly Lys Asn Gln Thr Leu Ala Thr Ile Lys Ala	400	405	410	
aag gaa aat cag ctg agc cag atc ctc gcc cct aac aac tat tat cca				1299
Lys Glu Asn Gln Leu Ser Gln Ile Leu Ala Pro Asn Asn Tyr Tyr Pro	415	420	425	
tcc aaa aat tta gcc ccc ata gcc ctg aac gcc cag gac gac ttt tcc				1347
Ser Lys Asn Leu Ala Pro Ile Ala Leu Asn Ala Gln Asp Asp Phe Ser	430	435	440	445
tct acc ccc ata act atg aat tac aat cag ttc ctg gag ctg gaa aag				1395
Ser Thr Pro Ile Thr Met Asn Tyr Asn Gln Phe Leu Glu Leu Glu Lys	450	455	460	
acg aag cag ctg aga cta gac acc gat cag gtg tat gga aac ata gcg				1443
Thr Lys Gln Leu Arg Leu Asp Thr Asp Gln Val Tyr Gly Asn Ile Ala	465	470	475	
aca tat aac ttt gag aac ggc cgc gtg cgc gtc gac act ggg tca aac				1491
Thr Tyr Asn Phe Glu Asn Gly Arg Val Arg Val Asp Thr Gly Ser Asn	480	485	490	
tgg tct gaa gtt ctg ccg caa att caa gag aca acc gcc aga att atc				1539
Trp Ser Glu Val Leu Pro Gln Ile Gln Glu Thr Thr Ala Arg Ile Ile	495	500	505	
ttt aat ggg aag gac ttg aac ctt gtc gaa cgt aga att gcc gcc gtg				1587
Phe Asn Gly Lys Asp Leu Asn Leu Val Glu Arg Arg Ile Ala Ala Val	510	515	520	525
aac ccc agt gat cca ctc gag acg act aaa ccg gat atg aca ctg aaa				1635
Asn Pro Ser Asp Pro Leu Glu Thr Thr Lys Pro Asp Met Thr Leu Lys	530	535	540	
gag gct ctg aag att gcc ttc gga ttc aac gaa cct aat ggc aat ttg				1683
Glu Ala Leu Lys Ile Ala Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu	545	550	555	
cag tat cag ggg aaa gac atc aca gag ttt gat ttc aat ttc gat cag				1731
Gln Tyr Gln Gly Lys Asp Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln	560	565	570	
cag act tcc caa aat atc aaa aat cag ttg gca gag ctg aat gcc acc				1779
Gln Thr Ser Gln Asn Ile Lys Asn Gln Leu Ala Glu Leu Asn Ala Thr	575	580	585	
aat atc tac acg gtt ctc gat aaa atc aaa ctt aac gcc aag atg aac				1827
Asn Ile Tyr Thr Val Leu Asp Lys Ile Lys Leu Asn Ala Lys Met Asn	590	595	600	605

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ata ttg att cga gac aaa cgc ttc cac tac gac cgc aac aat ata gcc 1875
 Ile Leu Ile Arg Asp Lys Arg Phe His Tyr Asp Arg Asn Asn Ile Ala
 610 615 620

gta ggc gct gat gag tct gtc gtc aag gag gct cat agg gaa gtt atc 1923
 Val Gly Ala Asp Glu Ser Val Val Lys Glu Ala His Arg Glu Val Ile
 625 630 635

aac agc agt act gaa ggg ctg tta ctt aat atc gac aag gac att cgg 1971
 Asn Ser Ser Thr Glu Gly Leu Leu Asn Ile Asp Lys Asp Ile Arg
 640 645 650

aag atc ctg tcc ggg tat atc gtg gag atc gag gat acc gag ggc ctg 2019
 Lys Ile Leu Ser Gly Tyr Ile Val Glu Ile Glu Asp Thr Glu Gly Leu
 655 660 665

aag gaa gtc att aac gac cgc tat gat atg ctg aac att tcc agc tta 2067
 Lys Glu Val Ile Asn Asp Arg Tyr Asp Met Leu Asn Ile Ser Ser Leu
 670 675 680 685

cga cag gac ggt aag aca ttt att gac ttt aaa aag tat aac gac aag 2115
 Arg Gln Asp Gly Lys Thr Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys
 690 695 700

cta ccc ctg tac att tcc aac cca aat tac aaa gtt aat gtg tat gct 2163
 Leu Pro Leu Tyr Ile Ser Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala
 705 710 715

gta acc aag gag aac aca atc atc aat cca agc gag aac ggc gat acc 2211
 Val Thr Lys Glu Asn Thr Ile Ile Asn Pro Ser Glu Asn Gly Asp Thr
 720 725 730

agc aca aat gga atc aaa aag atc ctt ata ttt agt aaa aaa ggc tac 2259
 Ser Thr Asn Gly Ile Lys Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr
 735 740 745

gag atc ggt tgaggatcc 2277
 Glu Ile Gly
 750

<210> 8

<211> 752

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TPA/synthetic antigen fusion protein

<400> 8

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Ala Val Phe Val Ser Pro Ser Glu Val Lys Gln Glu Asn Arg Leu Leu

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20	25	30
Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu Leu Gly Tyr Tyr Phe Ser 35 40 45		
Asp Leu Asn Phe Gln Ala Pro Met Val Val Thr Ser Ser Thr Thr Gly 50 55 60		
Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu Asn Ile Pro Ser Glu Asn 65 70 75 80		
Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly Phe Ile Lys Val Lys Lys 85 90 95		
Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala Asp Asn His Val Thr Met 100 105 110		
Trp Val Asp Asp Gln Glu Val Ile Asn Lys Ala Ser Asn Ser Asn Lys 115 120 125		
Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln Ile Lys Ile Gln Tyr Gln 130 135 140		
Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp Phe Lys Leu Tyr Trp Thr 145 150 155 160		
Asp Ser Gln Asn Lys Lys Glu Val Ile Ser Ser Asp Asn Leu Gln Leu 165 170 175		
Pro Glu Leu Lys Gln Lys Ser Ser Asn Thr Ser Ala Gly Pro Thr Val 180 185 190		
Pro Asp Arg Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly 195 200 205		
Tyr Thr Val Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile 210 215 220		
Ser Asn Ile His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro 225 230 235 240		
Glu Lys Trp Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val 245 250 255		
Thr Gly Arg Ile Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu 260 265 270		

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Val Ala Ala Tyr Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu
 275 280 285

Ser Lys Asn Glu Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg
 290 295 300

Thr Ile Ser Lys Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val
 305 310 315 320

His Gly Asn Ala Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser
 325 330 335

Val Ser Ala Gly Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp
 340 345 350

His Ser Leu Ser Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly
 355 360 365

Leu Asn Thr Ala Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val
 370 375 380

Asn Thr Gly Thr Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu
 385 390 395 400

Val Leu Gly Lys Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn
 405 410 415

Gln Leu Ser Gln Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn
 420 425 430

Leu Ala Pro Ile Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro
 435 440 445

Ile Thr Met Asn Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln
 450 455 460

Leu Arg Leu Asp Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn
 465 470 475 480

Phe Glu Asn Gly Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu
 485 490 495

Val Leu Pro Gln Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly
 500 505 510

Lys Asp Leu Asn Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser
 515 520 525

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Asp Pro Leu Glu Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu
530 535 540

Lys Ile Ala Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln
545 550 555 560

Gly Lys Asp Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser
565 570 575

Gln Asn Ile Lys Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr
580 585 590

Thr Val Leu Asp Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile
595 600 605

Arg Asp Lys Arg Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala
610 615 620

Asp Glu Ser Val Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser
625 630 635 640

Thr Glu Gly Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu
645 650 655

Ser Gly Tyr Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val
660 665 670

Ile Asn Asp Arg Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp
675 680 685

Gly Lys Thr Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu
690 695 700

Tyr Ile Ser Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys
705 710 715 720

Glu Asn Thr Ile Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn
725 730 735

Gly Ile Lys Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
740 745 750

<210> 9

<211> 2418

<212> DNA

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<213> Artificial Sequence

<220>

<223> Synthetic coding region for Human TPA/synthetic antigen fusion protein

<220>

<221> CDS

<222> (13) .. (2409)

<223>

<400> 9

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1 5 10	
ctg tgt gga gca gtc ttc gtt tgc ccc agc gcc ggc ggg cat ggg gac	99
Leu Cys Gly Ala Val Phe Val Ser Pro Ser Ala Gly Gly His Gly Asp	
15 20 25	
gtt ggc atg cat gtg aaa gaa aag gag aaa aac aag gac gaa aac aag	147
Val Gly Met His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys	
30 35 40 45	
cgt aaa gac gaa gaa cgt aat aaa aca cag gag gaa cac tta aag gag	195
Arg Lys Asp Glu Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu	
50 55 60	
atc atg aag cac ata gta aag att gag gta aaa ggc gaa gag gct gta	243
Ile Met Lys His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val	
65 70 75	
aag aag gag gca gca gaa aaa ctg ttg gag aag gtg cct tct gac gtc	291
Lys Lys Glu Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val	
80 85 90	
tta gag atg tat aag gcc atc ggc ggt aag atc tat atc gtg gac gga	339
Leu Glu Met Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly	
95 100 105	
gac atc act aaa cac ata tct ctc gaa gct ctc tcc gag gac aag aaa	387
Asp Ile Thr Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys	
110 115 120 125	
aag att aaa gac atc tac ggg aag gat gcc tta ttg cac gag cac tac	435
Lys Ile Lys Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr	
130 135 140	
gtt tac gca aag gag ggc tat gag ccc gtg ctc gtt att cag agt agt	483
Val Tyr Ala Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser	
145 150 155	
gag gac tac gtc gag aat acc gag aaa gct ctg aat gtg tat tac gag	531
Glu Asp Tyr Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu	

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160	165	170	
atc gga aag att ctg tcc cgg gac atc ctg tcc aaa atc aac cag cca Ile Gly Lys Ile Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro 175 180 185			579
tac cag aaa ttc ctt gat gtt ctt aac aca atc aaa aac gcg tca gat Tyr Gln Lys Phe Leu Asp Val Leu Asn Thr Ile Lys Asn Ala Ser Asp 190 195 200 205			627
agc gac ggg cag gat ctt ctg ttt aca aat caa ctc aag gaa cac ccc Ser Asp Gly Gln Asp Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro 210 215 220			675
act gat ttc agc gtg gag ttc ctc gag cag aat tct aac gaa gtc cag Thr Asp Phe Ser Val Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln 225 230 235			723
gag gtg ttc gcc aag gca ttt gcg tac tat atc gaa ccc cag cat cgc Glu Val Phe Ala Lys Ala Phe Ala Tyr Tyr Ile Glu Pro Gln His Arg 240 245 250			771
gat gtg ctc cag ctg tac gcc ccg gag gca ttt aac tac atg gac aaa Asp Val Leu Gln Leu Tyr Ala Pro Glu Ala Phe Asn Tyr Met Asp Lys 255 260 265			819
ttc aat gaa cag gag att aat ctg tct ctg gag gaa ctg aaa gac cag Phe Asn Glu Gln Glu Ile Asn Leu Ser Leu Glu Glu Leu Lys Asp Gln 270 275 280 285			867
agg atg ctc tcc cgg tat gaa aag tgg gaa aag atc aaa cag cat tac Arg Met Leu Ser Arg Tyr Glu Lys Trp Glu Lys Ile Lys Gln His Tyr 290 295 300			915
cag cat tgg tcc gac tcc ctg tca gaa gag ggg cgc ggc ctg ttg aaa Gln His Trp Ser Asp Ser Leu Ser Glu Glu Gly Arg Gly Leu Leu Lys 305 310 315			963
aag ttg cag att ccc atc gag cct aag aaa gat gat ata ata cac tct Lys Leu Gln Ile Pro Ile Glu Pro Lys Lys Asp Asp Ile Ile His Ser 320 325 330			1011
cta agc cag gag gag aag gaa ctc ctg aag cgg ata caa atc gac tca Leu Ser Gln Glu Glu Lys Glu Leu Leu Lys Arg Ile Gln Ile Asp Ser 335 340 345			1059
tcc gat ttc ctt agc aca gaa gag aag gag ttt cta aaa aaa ctt cag Ser Asp Phe Leu Ser Thr Glu Glu Lys Glu Phe Leu Lys Lys Leu Gln 350 355 360 365			1107
ata gat att aga gat tca ctg agc gag gaa gag aag gag ctg ctc aac Ile Asp Ile Arg Asp Ser Leu Ser Glu Glu Glu Lys Glu Leu Leu Asn 370 375 380			1155
cga att caa gtc gat agt tcg aac ccc ttg tca gaa aaa gag aag gaa Arg Ile Gln Val Asp Ser Ser Asn Pro Leu Ser Glu Lys Glu Lys Glu 385 390 395			1203
ttc ctg aaa aag ttg aag ctc gac atc cag ccg tac gat att aat cag Phe Leu Lys Lys Leu Lys Leu Asp Ile Gln Pro Tyr Asp Ile Asn Gln 400 405 410			1251

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cgg cta caa gac acc ggc ggt ctg att gat agc ccc agc atc aac ctt Arg Leu Gln Asp Thr Gly Gly Leu Ile Asp Ser Pro Ser Ile Asn Leu 415 420 425	1299
gac gta cgg aag caa tat aag cgc gac att caa aat atc gac gcc cta Asp Val Arg Lys Gln Tyr Lys Arg Asp Ile Gln Asn Ile Asp Ala Leu 430 435 440 445	1347
tta cat caa tcc ata ggc tcc acg cta tac aat aaa atc tat cta tac Leu His Gln Ser Ile Gly Ser Thr Leu Tyr Asn Lys Ile Tyr Leu Tyr 450 455 460	1395
gaa aac atg aat att aac aat ctc acc gct aca ctg gga gcg gac ctg Glu Asn Met Asn Ile Asn Asn Leu Thr Ala Thr Leu Gly Ala Asp Leu 465 470 475	1443
gtc gat agt aca gac aac aca aag ata aac aga ggt att ttc aac gaa Val Asp Ser Thr Asp Asn Thr Lys Ile Asn Arg Gly Ile Phe Asn Glu 480 485 490	1491
ttc aaa aag aac ttt aag tat tgc atc agc agt aac tat atg att gtt Phe Lys Lys Asn Phe Lys Tyr Ser Ile Ser Ser Asn Tyr Met Ile Val 495 500 505	1539
gac atc aat gaa cgg ccc gca tta gac aat gag agg ttg aag tgg aga Asp Ile Asn Glu Arg Pro Ala Leu Asp Asn Glu Arg Leu Lys Trp Arg 510 515 520 525	1587
att caa ctg agt cct gat act agg gcc ggc tat ctg gag aac ggg aaa Ile Gln Leu Ser Pro Asp Thr Arg Ala Gly Tyr Leu Glu Asn Gly Lys 530 535 540	1635
ctg atc tta cag cga aac atc ggg ctg gag atc aag gat gtg cag att Leu Ile Leu Gln Arg Asn Ile Gly Leu Glu Ile Lys Asp Val Gln Ile 545 550 555	1683
atc aag cag agc gaa aaa gaa tac att cgc atc gac gcc aag gtg gtg Ile Lys Gln Ser Glu Lys Glu Tyr Ile Arg Ile Asp Ala Lys Val Val 560 565 570	1731
cct aag tca aag atc gat acc aag atc cag gaa gct cag ctc aac att Pro Lys Ser Lys Ile Asp Thr Lys Ile Gln Glu Ala Gln Leu Asn Ile 575 580 585	1779
aac cag gag tgg aat aaa gct ctt ggt ctg cca aaa tac acc aaa ctt Asn Gln Glu Trp Asn Lys Ala Leu Gly Leu Pro Lys Tyr Thr Lys Leu 590 595 600 605	1827
atc acc ttt aat gtg cac aac agg tat gcc tct aat atc gtc gag tca Ile Thr Phe Asn Val His Asn Arg Tyr Ala Ser Asn Ile Val Glu Ser 610 615 620	1875
gca tac ctg att ctc aat gaa tgg aag aac aat att cag tct gac ctg Ala Tyr Leu Ile Leu Asn Glu Trp Lys Asn Asn Ile Gln Ser Asp Leu 625 630 635	1923
atc aag aag gtc acg aat tat ctg gtg gac gga aat ggc aga ttc gtg Ile Lys Lys Val Thr Asn Tyr Leu Val Asp Gly Asn Gly Arg Phe Val 640 645 650	1971
ttc acc gac ata act ttg cca aac att gcc gag caa tac act cat cag Phe Thr Asp Ile Thr Leu Pro Asn Ile Ala Glu Gln Tyr Thr His Gln	2019

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655	660	665	
gat gaa att tac gag Asp Glu Ile Tyr Glu 670	caa gtc cac tcc Gln Val His Ser 675	aaa ggt ctg tat gtt cca gag Lys Gly Leu Tyr Val Pro Glu 680	2067
tca aga tcg att ctg Ser Arg Ser Ile Leu 690	ctc cat ggt cca Leu His Gly Pro 695	aaa ggg gtt gag ctt cga Lys Gly Val Glu Leu Arg 700	2115
aac gat tct gag gga Asn Asp Ser Glu Gly 705	ttt atc gct gac Phe Ile Ala Asp 710	ttt gga gcc gct gtg gat gac Gly Ala Ala Val Asp Asp 715	2163
tac gcc gga tac ctg Tyr Ala Gly Tyr Leu 720	ttg gat aag aat Leu Asp Lys Asn 725	cag tct gat ctc gtg aca aat Gln Ser Asp Leu Val Thr Asn 730	2211
agc aaa aaa ttc ata Ser Lys Lys Phe Ile 735	gat att ttc aag Asp Ile Phe Lys 740	gag gaa ggg agt aac ctg act Glu Glu Gly Ser Asn Leu Thr 745	2259
tcc tat ggc cgc acg Ser Tyr Gly Arg Thr 750	aac gag gct gaa Asn Glu Ala Glu 755	ttt ttt gcg gaa gcc ttt aga Phe Phe Ala Glu Ala Phe Arg 760	2307
ott atg cac agc acc Leu Met His Ser Thr 770	gac cat gct gaa Asp His Ala Glu 775	agg ttg aag gtg caa aag aat Arg Leu Lys Val Gln Lys Asn 780	2355
gcc cct aaa acc ttc Ala Pro Lys Thr Phe 785	cag ttc ata aat Gln Phe Ile Asn 790	gac cag atc aag ttc atc atc Asp Gln Ile Lys Phe Ile Ile 795	2403
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<210> 10

<211> 799

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TPA/synthetic antigen fusion protein

<400> 10

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Ala	Val	Phe	Val	Ser	Pro	Ser	Ala	Gly	Gly	His	Gly	Asp	Val	Gly	Met
			20					25					30		

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His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp
 35 40 45

Glu Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu Ile Met Lys
 50 55 60

His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val Lys Lys Glu
 65 70 75 80

Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val Leu Glu Met
 85 90 95

Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr
 100 105 110

Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys
 115 120 125

Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr Val Tyr Ala
 130 135 140

Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser Glu Asp Tyr
 145 150 155 160

Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys
 165 170 175

Ile Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys
 180 185 190

Phe Leu Asp Val Leu Asn Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly
 195 200 205

Gln Asp Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro Thr Asp Phe
 210 215 220

Ser Val Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln Glu Val Phe
 225 230 235 240

Ala Lys Ala Phe Ala Tyr Tyr Ile Glu Pro Gln His Arg Asp Val Leu
 245 250 255

Gln Leu Tyr Ala Pro Glu Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu
 260 265 270

Gln Glu Ile Asn Leu Ser Leu Glu Glu Leu Lys Asp Gln Arg Met Leu
 275 280 285

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Ser Arg Tyr Glu Lys Trp Glu Lys Ile Lys Gln His Tyr Gln His Trp
 290 295 300

Ser Asp Ser Leu Ser Glu Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln
 305 310 315 320

Ile Pro Ile Glu Pro Lys Lys Asp Asp Ile Ile His Ser Leu Ser Gln
 325 330 335

Glu Glu Lys Glu Leu Leu Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe
 340 345 350

Leu Ser Thr Glu Glu Lys Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile
 355 360 365

Arg Asp Ser Leu Ser Glu Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln
 370 375 380

Val Asp Ser Ser Asn Pro Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys
 385 390 395 400

Lys Leu Lys Leu Asp Ile Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln
 405 410 415

Asp Thr Gly Gly Leu Ile Asp Ser Pro Ser Ile Asn Leu Asp Val Arg
 420 425 430

Lys Gln Tyr Lys Arg Asp Ile Gln Asn Ile Asp Ala Leu Leu His Gln
 435 440 445

Ser Ile Gly Ser Thr Leu Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met
 450 455 460

Asn Ile Asn Asn Leu Thr Ala Thr Leu Gly Ala Asp Leu Val Asp Ser
 465 470 475 480

Thr Asp Asn Thr Lys Ile Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys
 485 490 495

Asn Phe Lys Tyr Ser Ile Ser Ser Asn Tyr Met Ile Val Asp Ile Asn
 500 505 510

Glu Arg Pro Ala Leu Asp Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu
 515 520 525

Ser Pro Asp Thr Arg Ala Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu

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530	535	540
Gln Arg Asn Ile Gly Leu Glu Ile Lys Asp Val Gln Ile Ile Lys Gln 545 550 555 560		
Ser Glu Lys Glu Tyr Ile Arg Ile Asp Ala Lys Val Val Pro Lys Ser 565 570 575		
Lys Ile Asp Thr Lys Ile Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu 580 585 590		
Trp Asn Lys Ala Leu Gly Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe 595 600 605		
Asn Val His Asn Arg Tyr Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu 610 615 620		
Ile Leu Asn Glu Trp Lys Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys 625 630 635 640		
Val Thr Asn Tyr Leu Val Asp Gly Asn Gly Arg Phe Val Phe Thr Asp 645 650 655		
Ile Thr Leu Pro Asn Ile Ala Glu Gln Tyr Thr His Gln Asp Glu Ile 660 665 670		
Tyr Glu Gln Val His Ser Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser 675 680 685		
Ile Leu Leu His Gly Pro Ser Lys Gly Val Glu Leu Arg Asn Asp Ser 690 695 700		
Glu Gly Phe Ile Ala Asp Phe Gly Ala Ala Val Asp Asp Tyr Ala Gly 705 710 715 720		
Tyr Leu Leu Asp Lys Asn Gln Ser Asp Leu Val Thr Asn Ser Lys Lys 725 730 735		
Phe Ile Asp Ile Phe Lys Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly 740 745 750		
Arg Thr Asn Glu Ala Glu Phe Phe Ala Glu Ala Phe Arg Leu Met His 755 760 765		
Ser Thr Asp His Ala Glu Arg Leu Lys Val Gln Lys Asn Ala Pro Lys 770 775 780		

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gttattcatt ctggatagtc aataaataga ttacgggttat gttagtattt ttttaaata 240

atagtattaa atagtggaat gcaaatgata aatgggcttt aaacaaaact aatgaaataa 300

tctacaaatg gaatttctcc agtttttagat taaaccatac caaaaaaatc acactgtcaa 360

gaaaaatgat agaatcccta cactaattaa cataaccaa ttggtagtta taggtagaaa 420

cttattttatt tctataatac catgcaaaaa acaactaaa tattctgttc catactattt 480

tagtaaatta tttagcaagt aaattttggg gtataaaca agtttatctt aatataaaaa 540

attactttac ttttatacag attaaaatga aaaatTTTTT atgacaagaa atattgcctt 600

taatttatga ggaaataagt aaaattttct acatacttta ttttattggt gaaatgttca 660

cttataaaaa aggagagatt aaat atg aat ata aaa aaa gaa ttt ata aaa 711

Met Asn Ile Lys Lys Glu Phe Ile Lys
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gta att agt atg tca tgt tta gta aca gca att act ttg agt ggt ccc 759

Val Ile Ser Met Ser Cys Leu Val Thr Ala Ile Thr Leu Ser Gly Pro
 10 15 20 25

gtc ttt atc ccc ctt gta cag ggg gcg ggc ggt cat ggt gat gta ggt 807

Val Phe Ile Pro Leu Val Gln Gly Ala Gly Gly His Gly Asp Val Gly
 30 35 40

atg cac gta aaa gag aaa gag aaa aat aaa gat gag aat aag aga aaa 855

Met His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys Arg Lys
 45 50 55

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gat gaa gaa cga aat aaa aca cag gaa gag cat tta aag gaa atc atg Asp Glu Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu Ile Met 60 65 70	903
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gag gca gca gaa aag cta ctt gag aaa gta cca tct gat gtt tta gag Glu Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val Leu Glu 90 95 100 105	999
atg tat aaa gca att gga gga aag ata tat att gtg gat ggt gat att Met Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly Asp Ile 110 115 120	1047
aca aaa cat ata tct tta gaa gca tta tct gaa gat aag aaa aaa ata Thr Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys Lys Ile 125 130 135	1095
aaa gac att tat ggg aaa gat gct tta tta cat gaa cat tat gta tat Lys Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr Val Tyr 140 145 150	1143
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ctg tca aga tat gaa aaa tgg gaa aag ata aaa cag cac tat caa cac Leu Ser Arg Tyr Glu Lys Trp Glu Lys Ile Lys Gln His Tyr Gln His	1623

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300	305	310	
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cag att cct att gag cca aag aaa gat gac ata att cat tct tta tct Gln Ile Pro Ile Glu Pro Lys Lys Asp Asp Ile Ile His Ser Leu Ser 330 335 340 345			1719
caa gaa gaa aaa gag ctt cta aaa aga ata caa att gat agt agt gat Gln Glu Glu Lys Glu Leu Leu Lys Arg Ile Gln Ile Asp Ser Ser Asp 350 355 360			1767
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att cgt gat tct tta tct gaa gaa gaa aaa gag ctt tta aat aga ata Ile Arg Asp Ser Leu Ser Glu Glu Glu Lys Glu Leu Leu Asn Arg Ile 380 385 390			1863
cag gtg gat agt agt aat cct tta tct gaa aaa gaa aaa gag ttt tta Gln Val Asp Ser Ser Asn Pro Leu Ser Glu Lys Glu Lys Glu Phe Leu 395 400 405			1911
aaa aag ctg aaa ctt gat att caa cca tat gat att aat caa agg ttg Lys Lys Leu Lys Leu Asp Ile Gln Pro Tyr Asp Ile Asn Gln Arg Leu 410 415 420 425			1959
caa gat aca gga ggg tta att gat agt ccg tca att aat ctt gat gta Gln Asp Thr Gly Leu Ile Asp Ser Pro Ser Ile Asn Leu Asp Val 430 435 440			2007
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tta tca cca gat act cga gca gga tat tta gaa aat gga aag ctt ata Leu Ser Pro Asp Thr Arg Ala Gly Tyr Leu Glu Asn Gly Lys Leu Ile 540 545 550			2343

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caa tcc gaa aaa gaa tat ata agg att gat gcg aaa gta gtg cca aag Gln Ser Glu Lys Glu Tyr Ile Arg Ile Asp Ala Lys Val Val Pro Lys 570 575 580 585	2439
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tta ata ttg aat gaa tgg aaa aat aat att caa agt gat ctt ata aaa Leu Ile Leu Asn Glu Trp Lys Asn Asn Ile Gln Ser Asp Leu Ile Lys 635 640 645	2631
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gat att act ctc cct aat ata gct gaa caa tat aca cat caa gat gag Asp Ile Thr Leu Pro Asn Ile Ala Glu Gln Tyr Thr His Gln Asp Glu 670 675 680	2727
ata tat gag caa gtt cat tca aaa ggg tta tat gtt cca gaa tcc cgt Ile Tyr Glu Gln Val His Ser Lys Gly Leu Tyr Val Pro Glu Ser Arg 685 690 695	2775
tct ata tta ctc cat gga cct tca aaa ggt gta gaa tta agg aat gat Ser Ile Leu Leu His Gly Pro Ser Lys Gly Val Glu Leu Arg Asn Asp 700 705 710	2823
agt gag ggt ttt ata cac gaa ttt gga cat gct gtg gat gat tat gct Ser Glu Gly Phe Ile His Glu Phe Gly His Ala Val Asp Asp Tyr Ala 715 720 725	2871
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aaa ttc att gat att ttt aag gaa gaa ggg agt aat tta act tcg tat Lys Phe Ile Asp Ile Phe Lys Glu Glu Gly Ser Asn Leu Thr Ser Tyr 750 755 760	2967
ggg aga aca aat gaa gcg gaa ttt ttt gca gaa gcc ttt agg tta atg Gly Arg Thr Asn Glu Ala Glu Phe Phe Ala Glu Ala Phe Arg Leu Met 765 770 775	3015
cat tct acg gac cat gct gaa cgt tta aaa gtt caa aaa aat gct ccg His Ser Thr Asp His Ala Glu Arg Leu Lys Val Gln Lys Asn Ala Pro 780 785 790	3063
aaa act ttc caa ttt att aac gat cag att aag ttc att att aac tca Lys Thr Phe Gln Phe Ile Asn Asp Gln Ile Lys Phe Ile Ile Asn Ser	3111

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795	800	805	
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gatagtgtaa aagggtggcat tgccagaatg atattttatg tgttcgttag atatgaaggc			3291
aaaaacaatg atcctgacct agaacttaat gataatgtta ttaataattt aatgcctttt			3351
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tcaaaaaacc gaaatctgag ctcagatttc ggttttttga cgtatcttat acagatttgc			3531
aggttttaat ttcatttgct caatattaca aggatcagtt taaatgcaag tatgatgcac			3591
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			20					25					30		

Gly	Ala	Gly	Gly	His	Gly	Asp	Val	Gly	Met	His	Val	Lys	Glu	Lys	Glu
	35						40					45			

Lys	Asn	Lys	Asp	Glu	Asn	Lys	Arg	Lys	Asp	Glu	Glu	Arg	Asn	Lys	Thr
	50					55					60				

Gln	Glu	Glu	His	Leu	Lys	Glu	Ile	Met	Lys	His	Ile	Val	Lys	Ile	Glu
65					70					75					80

Val	Lys	Gly	Glu	Glu	Ala	Val	Lys	Lys	Glu	Ala	Ala	Glu	Lys	Leu	Leu
				85					90					95	

Glu	Lys	Val	Pro	Ser	Asp	Val	Leu	Glu	Met	Tyr	Lys	Ala	Ile	Gly	Gly
			100					105					110		

Lys	Ile	Tyr	Ile	Val	Asp	Gly	Asp	Ile	Thr	Lys	His	Ile	Ser	Leu	Glu
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115		120		125
Ala Leu Ser Glu Asp Lys	Lys Lys Ile Lys Asp	Ile Tyr Gly Lys Asp		
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Ala Leu Leu His Glu His Tyr Val Tyr Ala Lys Glu Gly Tyr Glu Pro				
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Val Leu Val Ile Gln Ser Ser Glu Asp Tyr Val Glu Asn Thr Glu Lys				
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Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys Ile Leu Ser Arg Asp Ile				
	180	185		190
Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys Phe Leu Asp Val Leu Asn				
	195	200		205
Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly Gln Asp Leu Leu Phe Thr				
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Asn Gln Leu Lys Glu His Pro Thr Asp Phe Ser Val Glu Phe Leu Glu				
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Gln Asn Ser Asn Glu Val Gln Glu Val Phe Ala Lys Ala Phe Ala Tyr				
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Tyr Ile Glu Pro Gln His Arg Asp Val Leu Gln Leu Tyr Ala Pro Glu				
	260	265		270
Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu Gln Glu Ile Asn Leu Ser				
	275	280		285
Leu Glu Glu Leu Lys Asp Gln Arg Met Leu Ser Arg Tyr Glu Lys Trp				
	290	295		300
Glu Lys Ile Lys Gln His Tyr Gln His Trp Ser Asp Ser Leu Ser Glu				
305	310	315		320
Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln Ile Pro Ile Glu Pro Lys				
	325	330		335
Lys Asp Asp Ile Ile His Ser Leu Ser Gln Glu Glu Lys Glu Leu Leu				
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Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe Leu Ser Thr Glu Glu Lys				
	355	360		365

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Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile Arg Asp Ser Leu Ser Glu
 370 375 380

Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln Val Asp Ser Ser Asn Pro
 385 390 395 400

Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys Lys Leu Lys Leu Asp Ile
 405 410 415

Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln Asp Thr Gly Gly Leu Ile
 420 425 430

Asp Ser Pro Ser Ile Asn Leu Asp Val Arg Lys Gln Tyr Lys Arg Asp
 435 440 445

Ile Gln Asn Ile Asp Ala Leu Leu His Gln Ser Ile Gly Ser Thr Leu
 450 455 460

Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met Asn Ile Asn Asn Leu Thr
 465 470 475 480

Ala Thr Leu Gly Ala Asp Leu Val Asp Ser Thr Asp Asn Thr Lys Ile
 485 490 495

Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys Asn Phe Lys Tyr Ser Ile
 500 505 510

Ser Ser Asn Tyr Met Ile Val Asp Ile Asn Glu Arg Pro Ala Leu Asp
 515 520 525

Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu Ser Pro Asp Thr Arg Ala
 530 535 540

Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu Gln Arg Asn Ile Gly Leu
 545 550 555 560

Glu Ile Lys Asp Val Gln Ile Ile Lys Gln Ser Glu Lys Glu Tyr Ile
 565 570 575

Arg Ile Asp Ala Lys Val Val Pro Lys Ser Lys Ile Asp Thr Lys Ile
 580 585 590

Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu Trp Asn Lys Ala Leu Gly
 595 600 605

Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe Asn Val His Asn Arg Tyr
 610 615 620

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Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu Ile Leu Asn Glu Trp Lys
625 630 635 640

Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys Val Thr Asn Tyr Leu Val
645 650 655

Asp Gly Asn Gly Arg Phe Val Phe Thr Asp Ile Thr Leu Pro Asn Ile
660 665 670

Ala Glu Gln Tyr Thr His Gln Asp Glu Ile Tyr Glu Gln Val His Ser
675 680 685

Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser Ile Leu Leu His Gly Pro
690 695 700

Ser Lys Gly Val Glu Leu Arg Asn Asp Ser Glu Gly Phe Ile His Glu
705 710 715 720

Phe Gly His Ala Val Asp Asp Tyr Ala Gly Tyr Leu Leu Asp Lys Asn
725 730 735

Gln Ser Asp Leu Val Thr Asn Ser Lys Lys Phe Ile Asp Ile Phe Lys
740 745 750

Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly Arg Thr Asn Glu Ala Glu
755 760 765

Phe Phe Ala Glu Ala Phe Arg Leu Met His Ser Thr Asp His Ala Glu
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Arg Leu Lys Val Gln Lys Asn Ala Pro Lys Thr Phe Gln Phe Ile Asn
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<213> Artificial Sequence

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antigen fusion protein

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ctg tgt gga gca gtc ttc gtt tgc ccc agc gcc ggc ggg cat ggg gac      99
Leu Cys Gly Ala Val Phe Val Ser Pro Ser Ala Gly Gly His Gly Asp
  15              20              25

gtt ggc atg cat gtg aaa gaa aag gag aaa aac aag gac gaa aac aag      147
Val Gly Met His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys
  30              35              40              45

cgt aaa gac gaa gaa cgt aat aaa aca cag gag gaa cac tta aag gag      195
Arg Lys Asp Glu Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu
        50              55              60

atc atg aag cac ata gta aag att gag gta aaa ggc gaa gag gct gta      243
Ile Met Lys His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val
        65              70              75

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Lys Lys Glu Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val
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tta gag atg tat aag gcc atc ggc ggt aag atc tat atc gtg gac gga      339
Leu Glu Met Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly
        95              100              105

gac atc act aaa cac ata tct ctc gaa gct ctc tcc gag gac aag aaa      387
Asp Ile Thr Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys
  110              115              120              125

aag att aaa gac atc tac ggg aag gat gcc tta ttg cac gag cac tac      435
Lys Ile Lys Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr
        130              135              140

gtt tac gca aag gag ggc tat gag ccc gtg ctc gtt att cag agt agt      483
Val Tyr Ala Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser
        145              150              155

gag gac tac gtc gag aat acc gag aaa gct ctg aat gtg tat tac gag      531
Glu Asp Tyr Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu
        160              165              170

atc gga aag att ctg tcc cgg gac atc ctg tcc aaa atc aac cag cca      579
Ile Gly Lys Ile Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro
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act Thr	gat Asp	ttc Phe	agc Ser	gtg Val	gag Glu	ttc Phe	ctc Leu	gag Glu	cag Gln	aat Asn	tct Ser	aac Asn	gaa Glu	gtc Val	cag Gln	723
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ttc Phe	aat Asn	gaa Glu	cag Gln	gag Glu	att Ile	aat Asn	ctg Leu	tct Ser	ctg Leu	gag Glu	gaa Glu	ctg Leu	aaa Lys	gac Asp	cag Gln	867
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cag Gln	cat His	tgg Trp	tcc Ser	gac Asp	tcc Ser	ctg Leu	tca Ser	gaa Glu	gag Glu	ggg Gly	cgc Arg	ggc Gly	ctg Leu	ttg Leu	aaa Lys	963
aag Lys	ttg Leu	cag Gln	att Ile	ccc Pro	atc Ile	gag Glu	cct Pro	aag Lys	aaa Lys	gat Asp	gat Asp	ata Ile	ata Ile	cac His	tct Ser	1011
cta Leu	agc Ser	cag Gln	gag Glu	gag Glu	aag Lys	gaa Glu	ctc Leu	ctg Leu	aag Lys	cgg Arg	ata Ile	caa Gln	atc Ile	gac Asp	tca Ser	1059
tcc Ser	gat Asp	ttc Phe	ctt Leu	agc Ser	aca Thr	gaa Glu	gag Glu	aag Lys	gag Glu	ttt Phe	cta Leu	aaa Lys	aaa Lys	ctt Leu	cag Gln	1107
ata Ile	gat Asp	att Ile	aga Arg	gat Asp	tca Ser	ctg Leu	agc Ser	gag Glu	gaa Glu	gag Glu	aag Lys	gag Glu	ctg Leu	ctc Leu	aac Asn	1155
cga Arg	att Ile	caa Gln	gtc Val	gat Asp	agt Ser	tcg Ser	aac Asn	ccc Pro	ttg Leu	tca Ser	gaa Glu	aaa Lys	gag Glu	aag Lys	gaa Glu	1203
ttc Phe	ctg Leu	aaa Lys	aag Lys	ttg Leu	aag Lys	ctc Leu	gac Asp	atc Ile	cag Gln	ccg Pro	tac Tyr	gat Asp	att Ile	aat Asn	cag Gln	1251
cgg Arg	cta Leu	caa Gln	gac Asp	acc Thr	ggc Gly	ggt Gly	ctg Leu	att Ile	gat Asp	agc Ser	ccc Pro	agc Ser	atc Ile	aac Asn	ctt Leu	1299
gac Asp	gta Val	cgg Arg	aag Lys	caa Gln	tat Tyr	aag Lys	cgc Arg	gac Asp	att Ile	caa Gln	aat Asn	atc Ile	gac Asp	gcc Ala	cta Leu	1347

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Glu Asn Met Asn Ile Asn Asn Leu Thr Ala Thr Leu Gly Ala Asp Leu	
465 470 475	
gtc gat agt aca gac aac aca aag ata aac aga ggt att ttc aac gaa	1491
Val Asp Ser Thr Asp Asn Thr Lys Ile Asn Arg Gly Ile Phe Asn Glu	
480 485 490	
ttc aaa aag aac ttt aag tat tcg atc agc agt aac tat atg att gtt	1539
Phe Lys Lys Asn Phe Lys Tyr Ser Ile Ser Ser Asn Tyr Met Ile Val	
495 500 505	
gac atc aat gaa cgg ccc gca tta gac aat gag agg ttg aag tgg aga	1587
Asp Ile Asn Glu Arg Pro Ala Leu Asp Asn Glu Arg Leu Lys Trp Arg	
510 515 520 525	
att caa ctg agt cct gat act agg gcc ggc tat ctg gag aac ggg aaa	1635
Ile Gln Leu Ser Pro Asp Thr Arg Ala Gly Tyr Leu Glu Asn Gly Lys	
530 535 540	
ctg atc tta cag cga aac atc ggg ctg gag atc aag gat gtg cag att	1683
Leu Ile Leu Gln Arg Asn Ile Gly Leu Glu Ile Lys Asp Val Gln Ile	
545 550 555	
atc aag cag agc gaa aaa gaa tac att cgc atc gac gcc aag gtg gtg	1731
Ile Lys Gln Ser Glu Lys Glu Tyr Ile Arg Ile Asp Ala Lys Val Val	
560 565 570	
tagggatcc	1740

<210> 14

<211> 573

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TPA/B. anthracis antigen fusion protein

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Ala Val Phe Val Ser Pro Ser Ala Gly Gly His Gly Asp Val Gly Met
20 25 30

His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp
35 40 45

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Glu Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu Ile Met Lys
 50 55 60

His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val Lys Lys Glu
 65 70 75 80

Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val Leu Glu Met
 85 90 95

Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr
 100 105 110

Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys
 115 120 125

Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr Val Tyr Ala
 130 135 140

Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser Glu Asp Tyr
 145 150 155 160

Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys
 165 170 175

Ile Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys
 180 185 190

Phe Leu Asp Val Leu Asn Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly
 195 200 205

Gln Asp Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro Thr Asp Phe
 210 215 220

Ser Val Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln Glu Val Phe
 225 230 235 240

Ala Lys Ala Phe Ala Tyr Tyr Ile Glu Pro Gln His Arg Asp Val Leu
 245 250 255

Gln Leu Tyr Ala Pro Glu Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu
 260 265 270

Gln Glu Ile Asn Leu Ser Leu Glu Glu Leu Lys Asp Gln Arg Met Leu
 275 280 285

Ser Arg Tyr Glu Lys Trp Glu Lys Ile Lys Gln His Tyr Gln His Trp
 290 295 300

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Ser Asp Ser Leu Ser Glu Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln
 305 310 315 320
 Ile Pro Ile Glu Pro Lys Lys Asp Asp Ile Ile His Ser Leu Ser Gln
 325 330 335
 Glu Glu Lys Glu Leu Leu Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe
 340 345 350
 Leu Ser Thr Glu Glu Lys Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile
 355 360 365
 Arg Asp Ser Leu Ser Glu Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln
 370 375 380
 Val Asp Ser Ser Asn Pro Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys
 385 390 395 400
 Lys Leu Lys Leu Asp Ile Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln
 405 410 415
 Asp Thr Gly Gly Leu Ile Asp Ser Pro Ser Ile Asn Leu Asp Val Arg
 420 425 430
 Lys Gln Tyr Lys Arg Asp Ile Gln Asn Ile Asp Ala Leu Leu His Gln
 435 440 445
 Ser Ile Gly Ser Thr Leu Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met
 450 455 460
 Asn Ile Asn Asn Leu Thr Ala Thr Leu Gly Ala Asp Leu Val Asp Ser
 465 470 475 480
 Thr Asp Asn Thr Lys Ile Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys
 485 490 495
 Asn Phe Lys Tyr Ser Ile Ser Ser Asn Tyr Met Ile Val Asp Ile Asn
 500 505 510
 Glu Arg Pro Ala Leu Asp Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu
 515 520 525
 Ser Pro Asp Thr Arg Ala Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu
 530 535 540
 Gln Arg Asn Ile Gly Leu Glu Ile Lys Asp Val Gln Ile Ile Lys Gln

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[illegible]

Ser Glu Lys Glu Tyr Ile Arg Ile Asp Ala Lys Val Val
565 570

<210> 15

<211> 753

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region for Human TPA/B. anthracis antigen fusion protein

<220>

<221> CDS

<222> (13) . . (744)

<223>

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      Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu
            1              5              10

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ctg tgt gga gca gtc ttc gtt tcg ccc agc gcc ggc ggg cat ggg gac 99
Leu Cys Gly Ala Val Phe Val Ser Pro Ser Ala Gly Gly His Gly Asp
15 20 25

gtt ggc atg cat gtg aaa gaa aag gag aaa aac aag gac gaa aac aag 147
Val Gly Met His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys
30 35 40 45

cgt aaa gac gaa gaa cgt aat aaa aca cag gag gaa cac tta aag gag 195
Arg Lys Asp Glu Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu
50 55 60

atc atg aag cac ata gta aag att gag gta aaa ggc gaa gag gct gta 243
Ile Met Lys His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val
65 70 75

aag aag gag gca gca gaa aaa ctg ttg gag aag gtg cct tct gac gtc 291
Lys Lys Glu Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val
80 85 90

tta gag atg tat aag gcc atc ggc ggt aag atc tat atc gtg gac gga 339
Leu Glu Met Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly
95 100 105

gac atc act aaa cac ata tct ctc gaa gct ctc tcc gag gac aaq aaa 387

-48-

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Asp Ile Thr Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys
110                      115                      120                      125

aag att aaa gac atc tac ggg aag gat gcc tta ttg cac gag cac tac      435
Lys Ile Lys Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr
                      130                      135                      140

gtt tac gca aag gag ggc tat gag ccc gtg ctc gtt att cag agt agt      483
Val Tyr Ala Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser
                      145                      150                      155

gag gac tac gtc gag aat acc gag aaa gct ctg aat gtg tat tac gag      531
Glu Asp Tyr Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu
                      160                      165                      170

atc gga aag att ctg tcc cgg gac atc ctg tcc aaa atc aac cag cca      579
Ile Gly Lys Ile Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro
                      175                      180                      185

tac cag aaa ttc ctt gat gtt ctt aac aca atc aaa aac gcg tca gat      627
Tyr Gln Lys Phe Leu Asp Val Leu Asn Thr Ile Lys Asn Ala Ser Asp
190                      195                      200                      205

agc gac ggg cag gat ctt ctg ttt aca aat caa ctc aag gaa cac ccc      675
Ser Asp Gly Gln Asp Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro
                      210                      215                      220

act gat ttc agc gtg gag ttc ctc gag cag aat tct aac gaa gtc cag      723
Thr Asp Phe Ser Val Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln
                      225                      230                      235

gag gtg ttc gcc aag gca ttt tgaggatcc      753
Glu Val Phe Ala Lys Ala Phe
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<210> 16

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TPA/B. anthracis antigen fusion protein

<400> 16

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Ala Val Phe Val Ser Pro Ser Ala Gly Gly His Gly Asp Val Gly Met
                20                      25                      30

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His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp
35                      40                      45

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Glu Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu Ile Met Lys
 50 55 60
 His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val Lys Lys Glu
 65 70 75 80
 Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val Leu Glu Met
 85 90 95
 Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr
 100 105 110
 Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys
 115 120 125
 Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr Val Tyr Ala
 130 135 140
 Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser Glu Asp Tyr
 145 150 155 160
 Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys
 165 170 175
 Ile Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys
 180 185 190
 Phe Leu Asp Val Leu Asn Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly
 195 200 205
 Gln Asp Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro Thr Asp Phe
 210 215 220
 Ser Val Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln Glu Val Phe
 225 230 235 240
 Ala Lys Ala Phe

<210> 17

<211> 1788

<212> DNA

<213> Artificial Sequence

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<220>

<223> Synthetic coding region for Human TPA/synthetic
antigen fusion protein

<220>

<221> CDS

<222> (13) .. (1779)

<223>

<400> 17

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ctg tgt gga gca gtc ttc gtt tcg ccc agc agc gct ggg cca act gtg	99
Leu Cys Gly Ala Val Phe Val Ser Pro Ser Ser Ala Gly Pro Thr Val	
15 20 25	
ccc gac aga gac aat gat gga atc cct gat agt cta gag gtt gag gga	147
Pro Asp Arg Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly	
30 35 40 45	
tac acg gta gat gtc aag aac aaa agg act ttt ctc tcg cct tgg atc	195
Tyr Thr Val Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile	
50 55 60	
tca aat atc cat gag aag aag ggg ctt acc aag tac aag tcc tcc ccc	243
Ser Asn Ile His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro	
65 70 75	
gag aag tgg tct acc gct tcc gat cca tat agc gat ttc gag aag gtc	291
Glu Lys Trp Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val	
80 85 90	
aca ggc cgg atc gat aaa cag gtg tct cca gag gct aga cac ccc ctg	339
Thr Gly Arg Ile Asp Lys Gln Val Ser Pro Glu Ala Arg His Pro Leu	
95 100 105	
gta gca gcc tac ccg att gta cac gtg gac atg gag aac atc att cta	387
Val Ala Ala Tyr Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu	
110 115 120 125	
agc aaa aac gag gac cag tcc aca caa aac act gac tcc gag acc cgc	435
Ser Lys Asn Glu Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg	
130 ' 135 140	
acc ata tct aaa cag acc agt act tca agg acc cac acc tct gaa gtg	483
Thr Ile Ser Lys Gln Thr Ser Thr Arg Thr His Thr Ser Glu Val	
145 150 155	
cac ggc aat gcg gaa gtc cat gca tcg ttt ttc gat att ggt ggc tcc	531
His Gly Asn Ala Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser	
160 165 170	
gtg tca gcc ggc ttt agc aat agc cag tcc tcg acg gtt gcc att gac	579
Val Ser Ala Gly Phe Ser Asn Ser Gln Ser Ser Thr Val Ala Ile Asp	

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175	180	185	
cac tca ctg tca tta gca ggt gag agg act tgg gct gaa act atg ggt His Ser Leu Ser Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly 190 195 200 205	627		
ctg aat acc gcc gat acg gcc cgg ctc aac gca aat att cgg tac gtc Leu Asn Thr Ala Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val 210 215 220	675		
aac aca ggg act gct cct ata tat aac gtg ctg cct acg aca agt ctt Asn Thr Gly Thr Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu 225 230 235	723		
gtc ctg ggc aaa cag cag acc ctc gca acc att aag gca aag gaa aat Val Leu Gly Lys Gln Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn 240 245 250	771		
cag ctg agc cag atc ctc gcc cct aac aac tat tat cca tcc aaa aat Gln Leu Ser Gln Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn 255 260 265	819		
tta gcc ccc ata gcc ctg aac gcc cag gac gac ttt tcc tct acc ccc Leu Ala Pro Ile Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro 270 275 280 285	867		
ata act atg aat tac aat cag ttc ctg gag ctg gaa aag acg aag cag Ile Thr Met Asn Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln 290 295 300	915		
ctg aga cta gac acc gat cag gtg tat gga aac ata gcg aca tat aac Leu Arg Leu Asp Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn 305 310 315	963		
ttt gag aac ggc cgc gtg cgc gtc gac act ggg tca cag tgg tct gaa Phe Glu Asn Gly Arg Val Arg Val Asp Thr Gly Ser Gln Trp Ser Glu 320 325 330	1011		
gtt ctg ccg caa att caa gag aca acc gcc aga att atc ttt aat ggg Val Leu Pro Gln Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly 335 340 345	1059		
aag gac ttg aac ctt gtc gaa cgt aga att gcc gcc gtg cag ccc agt Lys Asp Leu Asn Leu Val Glu Arg Arg Ile Ala Ala Val Gln Pro Ser 350 355 360 365	1107		
gat cca ctc gag acg act aaa ccg gat atg aca ctg aaa gag gct ctg Asp Pro Leu Glu Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu 370 375 380	1155		
aag att gcc ttc gga ttc aac gaa cct aat ggc aat ttg cag tat cag Lys Ile Ala Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln 385 390 395	1203		
ggg aaa gac atc aca gag ttt gat ttc aat ttc gat cag cag act tcc Gly Lys Asp Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser 400 405 410	1251		
caa aat atc aaa aat cag ttg gca gag ctg cag gcc acc aat atc tac Gln Asn Ile Lys Asn Gln Leu Ala Glu Leu Gln Ala Thr Asn Ile Tyr 415 420 425	1299		

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acg gtt ctc gat aaa atc aaa ctt aac gcc aag atg aac ata ttg att	1347
Thr Val Leu Asp Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile	
430 435 440 445	
cga gac aaa cgc ttc cac tac gac cgc aac aat ata gcc gta ggc gct	1395
Arg Asp Lys Arg Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala	
450 455 460	
gat gag tct gtc gtc aag gag gct cat agg gaa gtt atc cag agc agt	1443
Asp Glu Ser Val Val Lys Glu Ala His Arg Glu Val Ile Gln Ser Ser	
465 470 475	
act gaa ggg ctg tta ctt aat atc gac aag gac att cgg aag atc ctg	1491
Thr Glu Gly Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu	
480 485 490	
tcc ggg tat atc gtg gag atc gag gat acc gag ggc ctg aag gaa gtc	1539
Ser Gly Tyr Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val	
495 500 505	
att aac gac cgc tat gat atg ctg cag att tcc agc tta cga cag gac	1587
Ile Asn Asp Arg Tyr Asp Met Leu Gln Ile Ser Ser Leu Arg Gln Asp	
510 515 520 525	
ggt aag aca ttt att gac ttt aaa aag tat aac gac aag cta ccc ctg	1635
Gly Lys Thr Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu	
530 535 540	
tac att tcc aac cca aat tac aaa gtt aat gtg tat gct gta acc aag	1683
Tyr Ile Ser Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys	
545 550 555	
gag aac aca atc atc cag cca agc gag aac ggc gat acc agc aca aat	1731
Glu Asn Thr Ile Ile Gln Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn	
560 565 570	
gga atc aaa aag atc ctt ata ttt agt aaa aaa ggc tac gag atc ggt	1779
Gly Ile Lys Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly	
575 580 585	
tgaggatcc	1788

<210> 18

<211> 589

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TPA/synthetic antigen fusion protein

<400> 18

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Ala Val Phe Val Ser Pro Ser Ser Ala Gly Pro Thr Val Pro Asp Arg
 20 25 30

Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val
 35 40 45

Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile
 50 55 60

His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp
 65 70 75 80

Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg
 85 90 95

Ile Asp Lys Gln Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala
 100 105 110

Tyr Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn
 115 120 125

Glu Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg Thr Ile Ser
 130 135 140

Lys Gln Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn
 145 150 155 160

Ala Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala
 165 170 175

Gly Phe Ser Asn Ser Gln Ser Ser Thr Val Ala Ile Asp His Ser Leu
 180 185 190

Ser Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr
 195 200 205

Ala Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly
 210 215 220

Thr Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly
 225 230 235 240

Lys Gln Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser
 245 250 255

Gln Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro
 260 265 270

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Ile Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met
 275 280 285

Asn Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu
 290 295 300

Asp Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn
 305 310 315 320

Gly Arg Val Arg Val Asp Thr Gly Ser Gln Trp Ser Glu Val Leu Pro
 325 330 335

Gln Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu
 340 345 350

Asn Leu Val Glu Arg Arg Ile Ala Ala Val Gln Pro Ser Asp Pro Leu
 355 360 365

Glu Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala
 370 375 380

Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp
 385 390 395 400

Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile
 405 410 415

Lys Asn Gln Leu Ala Glu Leu Gln Ala Thr Asn Ile Tyr Thr Val Leu
 420 425 430

Asp Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys
 435 440 445

Arg Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser
 450 455 460

Val Val Lys Glu Ala His Arg Glu Val Ile Gln Ser Ser Thr Glu Gly
 465 470 475 480

Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr
 485 490 495

Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp
 500 505 510

Arg Tyr Asp Met Leu Gln Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr

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515	520	525
Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser		
530	535	540
Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr		
545	550	555
Ile Ile Gln Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys		
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		575
Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly		
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<212> DNA

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<220>

<223> Synthetic coding region for Human TPA/synthetic antigen fusion protein

<220>

<221> CDS

<222> (13) .. (2409)

<223>

<400> 19

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ctg tgt gga gca gtc ttc gtt tgc ccc agc gcc ggc ggg cat ggg gac	99
Leu Cys Gly Ala Val Phe Val Ser Pro Ser Ala Gly Gly His Gly Asp	
15 20 25	
gtt ggc atg cat gtg aaa gaa aag gag aaa aac aag gac gaa aac aag	147
Val Gly Met His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys	
30 35 40 45	
cgt aaa gac gaa gaa cgt cag aaa aca cag gag gaa cac tta aag gag	195
Arg Lys Asp Glu Arg Glu Arg Gln Lys Thr Gln Glu Glu His Leu Lys Glu	
50 55 60	
atc atg aag cac ata gta aag att gag gta aaa ggc gaa gag gct gta	243

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Ile	Met	Lys	His	Ile	Val	Lys	Ile	Glu	Val	Lys	Gly	Glu	Glu	Ala	Val		
			65					70						75			
aag	aag	gag	gca	gca	gaa	aaa	ctg	ttg	gag	aag	gtg	cct	tct	gac	gtc	291	
Lys	Lys	Glu	Ala	Ala	Glu	Lys	Leu	Leu	Glu	Lys	Val	Pro	Ser	Asp	Val		
		80					85					90					
tta	gag	atg	tat	aag	gcc	atc	ggc	ggg	aag	atc	tat	atc	gtg	gac	gga	339	
Leu	Glu	Met	Tyr	Lys	Ala	Ile	Gly	Gly	Lys	Ile	Tyr	Ile	Val	Asp	Gly		
	95					100					105						
gac	atc	act	aaa	cac	ata	tct	ctc	gaa	gct	ctc	tcc	gag	gac	aag	aaa	387	
Asp	Ile	Thr	Lys	His	Ile	Ser	Leu	Glu	Ala	Leu	Ser	Glu	Asp	Lys	Lys		
110					115					120					125		
aag	att	aaa	gac	atc	tac	ggg	aag	gat	gcc	tta	ttg	cac	gag	cac	tac	435	
Lys	Ile	Lys	Asp	Ile	Tyr	Gly	Lys	Asp	Ala	Leu	Leu	His	Glu	His	Tyr		
			130						135					140			
gtt	tac	gca	aag	gag	ggc	tat	gag	ccc	gtg	ctc	gtt	att	cag	agt	agt	483	
Val	Tyr	Ala	Lys	Glu	Gly	Tyr	Glu	Pro	Val	Leu	Val	Ile	Gln	Ser	Ser		
		145						150					155				
gag	gac	tac	gtc	gag	aat	acc	gag	aaa	gct	ctg	aat	gtg	tat	tac	gag	531	
Glu	Asp	Tyr	Val	Glu	Asn	Thr	Glu	Lys	Ala	Leu	Asn	Val	Tyr	Tyr	Glu		
		160					165					170					
atc	gga	aag	att	ctg	tcc	cgg	gac	atc	ctg	tcc	aaa	atc	aac	cag	cca	579	
Ile	Gly	Lys	Ile	Leu	Ser	Arg	Asp	Ile	Leu	Ser	Lys	Ile	Asn	Gln	Pro		
	175					180					185						
tac	cag	aaa	ttc	ctt	gat	gtt	ctt	aac	aca	atc	aaa	cag	gcg	tca	gat	627	
Tyr	Gln	Lys	Phe	Leu	Asp	Val	Leu	Asn	Thr	Ile	Lys	Gln	Ala	Ser	Asp		
190					195					200					205		
agc	gac	ggg	cag	gat	ctt	ctg	ttt	aca	aat	caa	ctc	aag	gaa	cac	ccc	675	
Ser	Asp	Gly	Gln	Asp	Leu	Leu	Phe	Thr	Asn	Gln	Leu	Lys	Glu	His	Pro		
			210						215					220			
act	gat	ttc	agc	gtg	gag	ttc	ctc	gag	cag	aat	tct	aac	gaa	gtc	cag	723	
Thr	Asp	Phe	Ser	Val	Glu	Phe	Leu	Glu	Gln	Asn	Ser	Asn	Glu	Val	Gln		
		225						230					235				
gag	gtg	ttc	gcc	aag	gca	ttt	gcg	tac	tat	atc	gaa	ccc	cag	cat	cgc	771	
Glu	Val	Phe	Ala	Lys	Ala	Phe	Ala	Tyr	Tyr	Ile	Glu	Pro	Gln	His	Arg		
		240					245					250					
gat	gtg	ctc	cag	ctg	tac	gcc	ccg	gag	gca	ttt	aac	tac	atg	gac	aaa	819	
Asp	Val	Leu	Gln	Leu	Tyr	Ala	Pro	Glu	Ala	Phe	Asn	Tyr	Met	Asp	Lys		
		255				260					265						
ttc	aat	gaa	cag	gag	att	cag	ctg	tct	ctg	gag	gaa	ctg	aaa	gac	cag	867	
Phe	Asn	Glu	Gln	Glu	Ile	Gln	Leu	Ser	Leu	Glu	Glu	Leu	Lys	Asp	Gln		
270					275					280					285		
agg	atg	ctc	tcc	cgg	tat	gaa	aag	tgg	gaa	aag	atc	aaa	cag	cat	tac	915	
Arg	Met	Leu	Ser	Arg	Tyr	Glu	Lys	Trp	Glu	Lys	Ile	Lys	Gln	His	Tyr		
			290					295					300				
cag	cat	tgg	tcc	gac	tcc	ctg	tca	gaa	gag	ggg	cgc	ggc	ctg	ttg	aaa	963	
Gln	His	Trp	Ser	Asp	Ser	Leu	Ser	Glu	Glu	Gly	Arg	Gly	Leu	Leu	Lys		
			305					310					315				

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aag ttg cag att ccc atc gag cct aag aaa gat gat ata ata cac tct Lys Leu Gln Ile Pro Ile Glu Pro Lys Lys Asp Asp Ile Ile His Ser 320 325 330	1011
cta agc cag gag gag aag gaa ctc ctg aag cgg ata caa atc gac tca Leu Ser Gln Glu Glu Lys Glu Leu Leu Lys Arg Ile Gln Ile Asp Ser 335 340 345	1059
tcc gat ttc ctt agc aca gaa gag aag gag ttt cta aaa aaa ctt cag Ser Asp Phe Leu Ser Thr Glu Glu Lys Glu Phe Leu Lys Lys Leu Gln 350 355 360 365	1107
ata gat att aga gat tca ctg agc gag gaa gag aag gag ctg ctc aac Ile Asp Ile Arg Asp Ser Leu Ser Glu Glu Glu Lys Glu Leu Leu Asn 370 375 380	1155
cga att caa gtc gat agt tcg aac ccc ttg tca gaa aaa gag aag gaa Arg Ile Gln Val Asp Ser Ser Asn Pro Leu Ser Glu Lys Glu Lys Glu 385 390 395	1203
ttc ctg aaa aag ttg aag ctc gac atc cag ccg tac gat att aat cag Phe Leu Lys Lys Leu Lys Leu Asp Ile Gln Pro Tyr Asp Ile Asn Gln 400 405 410	1251
cgg cta caa gac acc ggc ggt ctg att gat agc ccc agc atc aac ctt Arg Leu Gln Asp Thr Gly Glu Leu Ile Asp Ser Pro Ser Ile Asn Leu 415 420 425	1299
gac gta cgg aag caa tat aag cgc gac att caa aat atc gac gcc cta Asp Val Arg Lys Gln Tyr Lys Arg Asp Ile Gln Asn Ile Asp Ala Leu 430 435 440 445	1347
tta cat caa tcc ata ggc tcc acg cta tac aat aaa atc tat cta tac Leu His Gln Ser Ile Gly Ser Thr Leu Tyr Asn Lys Ile Tyr Leu Tyr 450 455 460	1395
gaa aac atg aat att aac cag ctc acc gct aca ctg gga gcg gac ctg Glu Asn Met Asn Ile Asn Gln Leu Thr Ala Thr Leu Gly Ala Asp Leu 465 470 475	1443
gtc gat agt aca gac aac aca aag ata aac aga ggt att ttc aac gaa Val Asp Ser Thr Asp Asn Thr Lys Ile Asn Arg Gly Ile Phe Asn Glu 480 485 490	1491
ttc aaa aag aac ttt aag tat tcg atc agc agt aac tat atg att gtt Phe Lys Lys Asn Phe Lys Tyr Ser Ile Ser Ser Asn Tyr Met Ile Val 495 500 505	1539
gac atc aat gaa cgg ccc gca tta gac aat gag agg ttg aag tgg aga Asp Ile Asn Glu Arg Pro Ala Leu Asp Asn Glu Arg Leu Lys Trp Arg 510 515 520 525	1587
att caa ctg agt cct gat act agg gcc ggc tat ctg gag aac ggg aaa Ile Gln Leu Ser Pro Asp Thr Arg Ala Gly Tyr Leu Glu Asn Gly Lys 530 535 540	1635
ctg atc tta cag cga aac atc ggg ctg gag atc aag gat gtg cag att Leu Ile Leu Gln Arg Asn Ile Gly Leu Glu Ile Lys Asp Val Gln Ile 545 550 555	1683
atc aag cag agc gaa aaa gaa tac att cgc atc gac gcc aag gtg gtg Ile Lys Gln Ser Glu Lys Glu Tyr Ile Arg Ile Asp Ala Lys Val Val	1731

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560	565	570	
cct aag tca aag atc gat acc aag atc cag gaa gct cag ctc aac att Pro Lys Ser Lys Ile Asp Thr Lys Ile Gln Glu Ala Gln Leu Asn Ile 575 580 585			1779
aac cag gag tgg aat aaa gct ctt ggt ctg cca aaa tac acc aaa ctt Asn Gln Glu Trp Asn Lys Ala Leu Gly Leu Pro Lys Tyr Thr Lys Leu 590 595 600 605			1827
atc acc ttt aat gtg cac aac agg tat gcc tct aat atc gtc gag tca Ile Thr Phe Asn Val His Asn Arg Tyr Ala Ser Asn Ile Val Glu Ser 610 615 620			1875
gca tac ctg att ctc aat gaa tgg aag aac aat att cag tct gac ctg Ala Tyr Leu Ile Leu Asn Glu Trp Lys Asn Asn Ile Gln Ser Asp Leu 625 630 635			1923
atc aag aag gtc acg aat tat ctg gtg gac gga aat ggc aga ttc gtg Ile Lys Lys Val Thr Asn Tyr Leu Val Asp Gly Asn Gly Arg Phe Val 640 645 650			1971
ttc acc gac ata act ttg cca aac att gcc gag caa tac act cat cag Phe Thr Asp Ile Thr Leu Pro Asn Ile Ala Glu Gln Tyr Thr His Gln 655 660 665			2019
gat gaa att tac gag caa gtc cac tcc aaa ggt ctg tat gtt cca gag Asp Glu Ile Tyr Glu Gln Val His Ser Lys Gly Leu Tyr Val Pro Glu 670 675 680 685			2067
tca aga tcg att ctg ctc cat ggt cca tcc aaa ggg gtt gag ctt cga Ser Arg Ser Ile Leu Leu His Gly Pro Ser Lys Gly Val Glu Leu Arg 690 695 700			2115
cag gat tct gag gga ttt atc gct gac ttt gga gcc gct gtg gat gac Gln Asp Ser Glu Gly Phe Ile Ala Asp Phe Gly Ala Ala Val Asp Asp 705 710 715			2163
tac gcc gga tac ctg ttg gat aag cag cag tct gat ctc gtg aca aat Tyr Ala Gly Tyr Leu Leu Asp Lys Gln Gln Ser Asp Leu Val Thr Asn 720 725 730			2211
agc aaa aaa ttc ata gat att ttc aag gag gaa ggg agt cag ctg act Ser Lys Lys Phe Ile Asp Ile Phe Lys Glu Glu Gly Ser Gln Leu Thr 735 740 745			2259
tcc tat ggc cgc acg aac gag gct gaa ttt ttt gcg gaa gcc ttt aga Ser Tyr Gly Arg Thr Asn Glu Ala Glu Phe Phe Ala Glu Ala Phe Arg 750 755 760 765			2307
ctt atg cac agc acc gac cat gct gaa agg ttg aag gtg caa aag aat Leu Met His Ser Thr Asp His Ala Glu Arg Leu Lys Val Gln Lys Asn 770 775 780			2355
gcc cct aaa acc ttc cag ttc ata aat gac cag atc aag ttc atc atc Ala Pro Lys Thr Phe Gln Phe Ile Asn Asp Gln Ile Lys Phe Ile Ile 785 790 795			2403
aac tct tgaggatcc Asn Ser			2418

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<210> 20

<211> 799

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TPA/synthetic antigen fusion protein

<400> 20

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15

Ala Val Phe Val Ser Pro Ser Ala Gly Gly His Gly Asp Val Gly Met
 20 25 30

His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp
 35 40 45

Glu Glu Arg Gln Lys Thr Gln Glu Glu His Leu Lys Glu Ile Met Lys
 50 55 60

His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val Lys Lys Glu
 65 70 75 80

Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val Leu Glu Met
 85 90 95

Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr
 100 105 110

Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys
 115 120 125

Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr Val Tyr Ala
 130 135 140

Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser Glu Asp Tyr
 145 150 155 160

Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys
 165 170 175

Ile Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys
 180 185 190

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Phe Leu Asp Val Leu Asn Thr Ile Lys Gln Ala Ser Asp Ser Asp Gly
 195 200 205

Gln Asp Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro Thr Asp Phe
 210 215 220

Ser Val Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln Glu Val Phe
 225 230 235 240

Ala Lys Ala Phe Ala Tyr Tyr Ile Glu Pro Gln His Arg Asp Val Leu
 245 250 255

Gln Leu Tyr Ala Pro Glu Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu
 260 265 270

Gln Glu Ile Gln Leu Ser Leu Glu Glu Leu Lys Asp Gln Arg Met Leu
 275 280 285

Ser Arg Tyr Glu Lys Trp Glu Lys Ile Lys Gln His Tyr Gln His Trp
 290 295 300

Ser Asp Ser Leu Ser Glu Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln
 305 310 315 320

Ile Pro Ile Glu Pro Lys Lys Asp Asp Ile Ile His Ser Leu Ser Gln
 325 330 335

Glu Glu Lys Glu Leu Leu Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe
 340 345 350

Leu Ser Thr Glu Glu Lys Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile
 355 360 365

Arg Asp Ser Leu Ser Glu Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln
 370 375 380

Val Asp Ser Ser Asn Pro Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys
 385 390 395 400

Lys Leu Lys Leu Asp Ile Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln
 405 410 415

Asp Thr Gly Gly Leu Ile Asp Ser Pro Ser Ile Asn Leu Asp Val Arg
 420 425 430

Lys Gln Tyr Lys Arg Asp Ile Gln Asn Ile Asp Ala Leu Leu His Gln

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435		440		445
Ser Ile Gly Ser Thr Leu Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met				
450		455		460
Asn Ile Asn Gln Leu Thr Ala Thr Leu Gly Ala Asp Leu Val Asp Ser				
465		470		475
Thr Asp Asn Thr Lys Ile Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys				
	485		490	495
Asn Phe Lys Tyr Ser Ile Ser Ser Asn Tyr Met Ile Val Asp Ile Asn				
	500		505	510
Glu Arg Pro Ala Leu Asp Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu				
	515		520	525
Ser Pro Asp Thr Arg Ala Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu				
	530		535	540
Gln Arg Asn Ile Gly Leu Glu Ile Lys Asp Val Gln Ile Ile Lys Gln				
	545		550	555
Ser Glu Lys Glu Tyr Ile Arg Ile Asp Ala Lys Val Val Pro Lys Ser				
	565		570	575
Lys Ile Asp Thr Lys Ile Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu				
	580		585	590
Trp Asn Lys Ala Leu Gly Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe				
	595		600	605
Asn Val His Asn Arg Tyr Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu				
	610		615	620
Ile Leu Asn Glu Trp Lys Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys				
	625		630	635
Val Thr Asn Tyr Leu Val Asp Gly Asn Gly Arg Phe Val Phe Thr Asp				
	645		650	655
Ile Thr Leu Pro Asn Ile Ala Glu Gln Tyr Thr His Gln Asp Glu Ile				
	660		665	670
Tyr Glu Gln Val His Ser Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser				
	675		680	685

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Ile Leu Leu His Gly Pro Ser Lys Gly Val Glu Leu Arg Gln Asp Ser
 690 695 700

Glu Gly Phe Ile Ala Asp Phe Gly Ala Ala Val Asp Asp Tyr Ala Gly
 705 710 715 720

Tyr Leu Leu Asp Lys Gln Gln Ser Asp Leu Val Thr Asn Ser Lys Lys
 725 730 735

Phe Ile Asp Ile Phe Lys Glu Glu Gly Ser Gln Leu Thr Ser Tyr Gly
 740 745 750

Arg Thr Asn Glu Ala Glu Phe Phe Ala Glu Ala Phe Arg Leu Met His
 755 760 765

Ser Thr Asp His Ala Glu Arg Leu Lys Val Gln Lys Asn Ala Pro Lys
 770 775 780

Thr Phe Gln Phe Ile Asn Asp Gln Ile Lys Phe Ile Ile Asn Ser
 785 790 795

<210> 21

<211> 2292

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region

<400> 21

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accggcaacc tggaggtgat ccaggccgag gtgaagcagg agaacaggct gctgaacgag	120
agcgagagca gcagccaggg cctgctgggc tactacttca gcgacctgaa cttccaggcc	180
cccatggtgg tgaccagcag caccaccggc gacctgagca tccccagcag cgagctggag	240
aacatcccca gcgagaacca gtacttcag agcgccatct ggagcggctt catcaaggtg	300
aagaagagcg acgagtacac cttcgccacc agcgccgaca accacgtgac catgtgggtg	360
gacgaccagg aggtgatcaa caaggccagc aacagcaaca agatcaggct ggagaagggc	420
aggctgtacc agatcaagat ccagtaccag agggagaacc ccaccgagaa gggcctggac	480
ttcaagctgt actggaccga cagccagaac aagaaggagg tgatcagcag cgacaacctg	540
cagctgcccg agctgaagca gaagagcagc aacagcagga agaagaggag caccagcgcc	600

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ggccccaccg tgcccgacag ggacaacgac ggcatccccg acagcctgga ggtggagggc 660
tacaccgtgg acgtgaagaa caagaggacc ttcctgagcc cctggatcag caacatccac 720
gagaagaagg gcctgaccaa gtacaagagc agccccgaga agtggagcac cgccagcgac 780
ccctacagcg acttcgagaa ggtgaccggc aggatcgaca agaacgtgag ccccgaggcc 840
aggcaccccc tgggtggccgc ctaccccatc gtgcacgtgg acatggagaa catcatcctg 900
agcaagaacg aggaccagag caccagaac accgacagcg agaccaggac catcagcaag 960
aacaccagca ccagcaggac ccacaccagc gaggtgcacg gcaacgccga ggtgcacgcc 1020
agcttcttcg acatcggcgg cagcgtgagc gccggcttca gcaacagcaa cagcagcacc 1080
gtggccatcg accacagcct gagcctggcc ggcgagagga cctgggccga gaccatgggc 1140
ctgaacaccg ccgacaccgc caggctgaac gccaacatca ggtacgtgaa caccggcacc 1200
gcccccatct acaacgtgct gccaccacc agcctggtgc tgggcaagaa ccagaccctg 1260
gccaccatca aggccaagga gaaccagctg agccagatcc tggcccccaa caactactac 1320
cccagcaaga acctggcccc catcgccctg aacgcccagg acgacttcag cagcaccccc 1380
atcaccatga actacaacca gttcctggag ctggagaaga ccaagcagct gaggtctggac 1440
accgaccagg tgtacggcaa catcgccacc tacaacttcg agaacggcag ggtgagggtg 1500
gacaccggca gcaactggag cgagggtgctg ccccgatcc aggagaccac cgccaggatc 1560
atcttcaacg gcaaggacct gaacctggtg gagaggagga tcgccgccgt gaacccagc 1620
gaccccttg agaccaccaa gcccgacatg accctgaagg aggccctgaa gatcgcttc 1680
ggcttcaacg agcccaacgg caacctgcag taccagggca aggacatcac cgagtctgac 1740
ttcaacttcg accagcagac cagccagaac atcaagaacc agctggccga gctgaacgcc 1800
accaacatct acaccgtgct ggacaagatc aagctgaacg ccaagatgaa catcctgatc 1860
agggacaaga ggttccacta cgacaggaac aacatcgccg tgggcgccga cgagagcgtg 1920
gtgaaggagg ccacagggg ggtgatcaac agcagcaccg agggcctgct gctgaacatc 1980
gacaaggaca tcaggaagat cctgagcggc tacatcgtgg agatcgagga caccgagggc 2040
ctgaaggagg tgatcaacga caggtagcag atgctgaaca tcagcagcct gaggcaggac 2100
ggcaagacct tcatcgactt caagaagtac aacgacaagc tgcccctgta catcagcaac 2160
cccaactaca aggtgaacgt gtacgccgtg accaaggaga acaccatcat caacccagc 2220
gagaacggcg acaccagcac caacggcatc aagaagatcc tgatcttcag caagaagggc 2280
tacgagatcg gc 2292

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<210> 22

<211> 2427

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region

<400> 22

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accctgagcg gccccgtgtt catccccctg gtgcagggcg ccggcggcca cggcgacgtg	120
ggcatgcacg tgaaggagaa ggagaagaac aaggacgaga acaaggaggaa ggacgaggag	180
aggaacaaga cccaggagga gcacctgaag gagatcatga agcacatcgt gaagatcgag	240
gtgaagggcg aggaggccgt gaagaaggag gccgccgaga agctgctgga gaaggtgccc	300
agcgacgtgc tggagatgta caaggccatc ggccggcaaga tctacatcgt ggacggcgac	360
atcaccaagc acatcagcct ggaggccctg agcgaggaca agaagaagat caaggacatc	420
tacggcaagg acgccctgct gcacgagcac tacgtgtacg ccaaggaggg ctacgagccc	480
gtgctggtga tccagagcag cgaggactac gtggagaaca ccgagaaggc cctgaacgtg	540
tactacgaga tcggcaagat cctgagcagg gacatcctga gcaagatcaa ccagccctac	600
cagaagttcc tggacgtgct gaacaccatc aagaacgcca gcgacagcga cggccaggac	660
ctgctgttca ccaaccagct gaaggagcac cccaccgact tcagcgtgga gttcctggag	720
cagaacagca acgaggtgca ggagggtgtt gcccaaggcct tcgcctacta catcgagccc	780
cagcacaggg acgtgctgca gctgtacgcc cccgaggcct tcaactacat ggacaagtgc	840
aacgagcagg agatcaacct gagcctggag gagctgaagg accagaggat gctgagcagg	900
tacgagaagt gggagaagat caagcagcac taccagcact ggagcgacag cctgagcgag	960
gagggcaggg gcctgctgaa gaagctgcag atccccatcg agcccaagaa ggacgacatc	1020
atccacagcc tgagccagga ggagaaggag ctgctgaaga ggatccagat cgacagcagc	1080
gaattcctga gcaccgagga gaaggagtgc ctgaagaagc tgcagatcga catcagggac	1140
agcctgagcg aggaggagaa ggagctgctg aacaggatcc aggtggacag cagcaacccc	1200
ctgagcgaga aggagaagga gttcctgaag aagctgaagc tggacatcca gccctacgac	1260
atcaaccaga ggctgcagga caccggcggc ctgatcgaca gcccagcat caacctggac	1320
gtgaggaagc agtacaagag ggacatccag aacatcgacg ccctgctgca ccagagcatc	1380
ggcagcacc tgatcaacaa gatctacctg tacgagaaca tgaacatcaa caacctgacc	1440
gccaccctgg gcgccgacct ggtggacagc accgacaaca ccaagatcaa caggggcac	1500
ttcaacgagt tcaagaagaa cttcaagtac agcatcagca gcaactacat gatcgtggac	1560

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atcaacgaga ggccccgcct ggacaacgag aggctgaagt ggaggatcca gctgagcccc 1620
gacaccaggg cgggtacct ggagaacggc aagctgatcc tgcagaggaa catcggcctg 1680
gagatcaagg acgtgcagat catcaagcag agcgagaagg agtacatcag gatcgacgcc 1740
aaggtggtgc ccaagagcaa gatcgacacc aagatccagg aggcccagct gaacatcaac 1800
caggagtgga acaaggccct gggcctgccc aagtacacca agctgatcac cttcaacgtg 1860
cacaacaggt acgccagcaa catcgtggag agcgccctacc tgatcctgaa cgagtggaag 1920
aacaacatcc agagcgacct gatcaagaag gtgaccaact acctggtgga cggcaacggc 1980
aggttcgtgt tcaccgacat caccctgccc aacatcgccg agcagtacac ccaccaggac 2040
gagatctacg agcagggtgca cagcaagggc ctgtacgtgc ccgagagcag gagcatcctg 2100
ctgcacggcc ccagcaaggg cgtggagctg aggaacgaca gcgagggctt catccacgag 2160
ttcgggcacg ccgtggacga ctacgccggc tacctgctgg acaagaacca gagcgacctg 2220
gtgaccaaca gcaagaagtt catcgacatc ttcaaggagg agggcagcaa cctgaccagc 2280
tacggcagga ccaacgaggc cgagttcttc gocgaggcct tcaggctgat gcacagcacc 2340
gaccacgccg agaggctgaa ggtgcagaag aacgccccca agaccttcca gttcatcaac 2400
gaccagatca agttcatcat caacagc 2427

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<210> 23

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region

<400> 23

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agcgaaagtt catcacaggg tcttctcgga tactacttca gtgacttgaa tttccaagca 180
ccaatggtgg tgactagtag caccacggc gatttgagca ttcccagctc tgagttggag 240
aacattccca gcgaaaatca gtacttcag tctgctatct ggtccggatt cattaaggtt 300
aaaaagtcg acgaatatac atttgctacc tcggcgata accatgtgac aatgtgggtg 360
gacgaccagg aagtgatcaa caaggcttca aactctaata aaatccggct cgagaagggg 420
aggctctacc agatcaaaat tcagtaccag cgggaaaacc ctacagaaaa aggactcgat 480

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ttcaagctgt actggacaga tagccaaaac aagaaagaag ttatcagctc agacaatctg	540
cagttacccg agctcaagca gaagagttct aattctagga agaaaagatc tacatccgca	600
gggccaaactg tgcccgcag agacaatgat ggaatccctg atagtctaga ggttgagggg	660
tacacggtag atgtcaagaa caaaaggact tttctctcgc cttggatata aaatatccat	720
gagaagaagg ggcttaccaa gtacaagtcc tcccccgaga agtggctctac cgcttccgat	780
ccatatagcg atttcgagaa ggtcacaggc cggatcgata aaaatgtgtc tccagaggct	840
agacaccccc tggtagcagc ctacccgatt gtacacgtgg acatggagaa catcattcta	900
agcaaaaacg aggaccagtc cacacaaaac actgactccg agaccgcac catatctaaa	960
aacaccagta cttcaaggac ccacacctct gaagtgcacg gcaatgcgga agtccatgca	1020
tcgtttttcg atattgggtg atccgtgtca gccggcttta gcaatagcaa ctccctcgacg	1080
gttgccattg accactcact gtcattagca ggtgagagga cttgggctga aactatgggt	1140
ctgaataccg ccgatacggc ccggctcaac gcaaatattc ggtacgtcaa cacagggact	1200
gtccttatat ataacgtgct gcctacgaca agtcttgtcc tgggcaaaaa tcagaccctc	1260
gcaaccatta aggcaaagga aaatcagctg agccagatcc tcgcccctaa caactattat	1320
ccatccaaaa atttagcccc catagccctg aacgcccgagg acgacttttc ctctaccccc	1380
ataactatga attacaatca gttcctggag ctggaaaaga cgaagcagct gagactagac	1440
accgatcagg tgtatggaaa catagcgaca tataactttg agaacggccg cgtgcgcgtc	1500
gacactgggt caaactggtc tgaagttctg ccgcaaattc aagagacaac cgccagaatt	1560
atctttaatg ggaaggactt gaaccttgct gaacgtagaa ttgccgccgt gaaccccagt	1620
gatccactcg agacgactaa accggatatg acactgaaag aggctctgaa gattgccttc	1680
ggattcaacg aacctaattg caatttgtag tatcagggga aagacatcac agagtttgat	1740
ttcaatttcg atcagcagac ttcccaaaat atcaaaaatc agttggcaga gctgaatgcc	1800
accaatatct acacggttct cgataaaatc aaacttaacg ccaagatgaa catattgatt	1860
cgagacaaac gcttccacta cgaccgcaac aatatagccg taggcgctga tgagtctgtc	1920
gtcaaggagg ctcatagggg agttatcaac agcagtactg aagggtgtt acttaatatc	1980
gacaaggaca ttcggaagat octgtccggg tatatcgtgg agatcgagga taccgagggc	2040
ctgaagggaag tcattaacga ccgctatgat atgctgaaca tttccagctt acgacaggac	2100
ggtaagacat ttattgactt taaaaagtat aacgacaagc taccctgtg catttccaac	2160
ccaaattaca aagttaatgt gtatgctgta accaaggaga acacaatcat caatccaagc	2220
gagaacggcg ataccagcac aaatggaatc aaaaagatcc ttatathtag taaaaaggc	2280
tacgagatcg gttga	2295

-67-

<210> 24

<211> 2292

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region

<400> 24

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atgaaaaaga ggaagggtgct gatccctctc atggccctgt ctaccatcct ggttagtagc      60
acaggggaacc tggaagtgat tcaggccgag gttaagcaag agaataggct gctcaacgag      120
tcagaatctt cgtcacaggg attattgggt tactatTTTT cggacctgaa tttccaggcc      180
ccaatggtcg ttacaagctc cacaacaggc gacctgtcta tccccagctc cgaattggag      240
aacatcccta gcgagaacca atactttcaa agcgctatTT ggtcaggctt cataaaagtg      300
aagaagtctg acgaatacac gtttgcaaca tctgccgata accacgtcac tatgtgggtc      360
gatgaccagg aagtcatcaa caaggctagt aatagcaaca aaatcagact ggagaaaggg      420
agattgtacc agatcaagat ccagtaccaa cgggaaaacc caacagagaa gggcctcgat      480
tttaaactgt attggactga ctctcagaat aagaaggaag tgattagcag cgacaattta      540
caattacccg agttgaaaca gaagagctct aattcaagga aaaagagatc tacctccgcc      600
ggaccaacag ttccagatag ggataatgat ggaatccctg actcactgga ggtcgagggt      660
tacaccgtgg acgtgaaaaa caaacgcact ttctatcac cctggatctc caacattcac      720
gagaagaagg gtctgactaa gtacaaatcc agcccagaga aatggagcac cgcaagtgat      780
ccttatagtg acttcgagaa ggtgacgggc cggatagaca agaacgtatc acccgaagct      840
cgtcatcctc tggtcgccgc ctaccctatt gtgcatgtgg acatggaaaa catcatcctg      900
agtaagaacg aagaccagag cactcagaac accgactccg agacacgaac gatatctaag      960
aatacatcca cctcacgcac tcataccagc gaagtgcacg gtaacgctga agtgcacgcg     1020
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gtagctattg accacagcct gagccttgcc ggagaaagga catgggcgga gactatgggc     1140
ctgaatacgg ctgatacggc acggctcaat gccaacatca gatacgtgaa caccgggaca     1200
gccctatTTT acaatgtgct cccaaccaca tcaactgtac tgggaaaaaa ccagacccta     1260
gctactatta aagcgaagaa aaatcagttg tcacagatac tggcacccaa caattattat     1320
ccaagcaaaa acctggcacc catcgcactc aatgcgcagg atgactttag tagtacaccc     1380
attacaatga actacaatca gttccttgag ctcgagaaga ccaagcaact gagactcgac     1440

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-68-

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actgaccagg tgtatggtaa tatcgccacc tacaacttcg aaaacggaag ggtgcgggta 1500
gatacgggct ccaactggtc ggaggtgtta cctcagatcc aggaaaccac cgcccgcat 1560
atthttcaacg gcaaggatct aaatctcgtt gagcgccgga tagcagctgt caatcccagt 1620
gatccgctcg aaaccaccaa gcccgacatg actttgaagg aagctcttaa gattgccttt 1680
gggtttaacg agcccaatgg gaatctgcag taccagggca aagatattac cgagtgtgat 1740
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cgagataagc gcttccatta tgatcgaaat aacatcgag ttggcgccga cgaatcagtt 1920
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ggaaagactt tcattgattt caagaaatac aacgataaac tcccgctgta tatctccaac 2160
ccaaattata aggtgaatgt gtacgctgtc accaaagaga ataccattat taacccgtct 2220
gagaatggcg acacctccac gaatgggata aaaaaatcc ttatcttcag taaaaaggc 2280
tacgagatcg gg 2292

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<210> 25

<211> 2292

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region

<400> 25

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atgaaaaaaaa ggaagggtgt gatccccctt atggcccttt ccaccatctt ggtatcctca 60
accggcaacc tggaggttat tcaagccgaa gtgaagcagg aaaatagact gctgaacgaa 120
tccgaatcta gttctcaggg tctgctgggc tactatttta gcgacctcaa tttccaggca 180
ccaatggtcg tgacttcgag caccacaggc gacttgagca ttccctcttc cgaactcgag 240
aacataccaa gcgagaatca gtatcttcag tcgcgaatct ggtcgggttt tatcaaagta 300
aaaaagagcg acgaatacac ttctcgctacg tcagccgata atcatgtgac catgtgggtg 360
gatgaccaag aggtcatcaa taaggcgagt aactctaaca agattcgact ggaaaaggga 420
cgcctctatc agattaagat tcagtaccag cgtgagaacc ccaactgaaa ggtctctggac 480

```

-69-

tttaagctgt attggacgga tagtcagaat aaaaaggagg tgatcagttc agacaacttg	540
caattgcctg agctgaaaca gaagtccagc aactctcgga agaagcgag tactagcgct	600
ggcccaacag tccccgaccg cgacaatgat gggattcccg attctttgga agtggaggga	660
tacacagtgg acgtgaagaa caagagaaca ttcctgagtc catggattag taatatccat	720
gagaaaaaag gtctaacc aaacaaaagc agcccagaga agtggccaac agcatcggat	780
ccttactccg atttcgagaa agttactggc aggattgaca agaacgtatc tccggaggcc	840
aggcatcctc tcgtcgccgc ttacccgacg gtccacgtcg acatggagaa catcatcctg	900
agtaagaatg aggatcaaag cactcagaat actgattccg agacacggac aatcagtaag	960
aatacctcaa cgagcaggac acacacctct gaagttcacg gcaatgccga ggtgcacgct	1020
tcattcttcg atatcgaggg atccgtgagc gcgggcttca gcaactctaa ctcttccact	1080
gtagcgatcg atcatagcct ctccctagcc ggagagcgga catgggctga gaccatgggg	1140
ttgaatactg cagatacagc aagactgaac gccaatatta ggtatgtgaa tacagggtacc	1200
gccccatct acaacgtcct tcctaccacc tcaactgggt taggcaaaaa tcagaccctc	1260
gccaccatta aggcaaaaga gaatcaactc tcacagatac tggcccaaaa caactattac	1320
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atcttcaatg gaaaagacct gaatcttggt gagcgcgaa tcgccgtgt gaatccttc	1620
gaccctctgg aaacgacgaa gcccgacatg actttgaaag aggcgctaaa aatcgctttt	1680
ggatttaatg aaccgaacgg caacttacia tatcaaggga aggacattac cgagttcgac	1740
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agagacaaga gatttcacta cgataggaat aacattgccg ttggagccga tgagtctgtg	1920
gtgaaagagg cacaccgga ggtcattaac tccagcactg aagggtctgt gctgaacatt	1980
gacaaggata ttagaaaaat cctgagcggg tacatcgttg agatcgaaga taccgaggga	2040
cttaaggaag ttataaacga ccgttatgac atgttaaaca tatcaagcct ccggcaggac	2100
ggtaagacat ttatagattt caagaaatac aacgataagc ttctctttta catctcaaat	2160
cccaactata aggtgaatgt ttatgcagta acaaaagaaa atacaattat taatccatcc	2220
gagaacggcg atacatctac taacgggata aaaaaaatcc tcatcttctc caagaaaggc	2280
tacgagatag gg	2292

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<210> 26

<211> 2430

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region

<400> 26

atgaacatca aaaaagagtt tataaagggtg attagcatga gctgcctggg cactgccatt	60
accctgagtg gccagtggt tatccctctc gtccaggggc ccggcgggca tggggacgtt	120
ggcatgcatg tgaaagaaaa ggagaaaaac aaggacgaaa acaagcgtaa agacgaagaa	180
cgtaataaaaa cacaggagga acacttaaag gagatcatga agcacatagt aaagattgag	240
gtaaaaggcg aagaggctgt aaagaaggag gcagcagaaa aactgttgga gaaggcgctt	300
tctgacgtct tagagatgta taaggccatc ggcggtgaga tctatatcgt ggacggagac	360
atcactaaac acatatctct cgaagctctc tccgaggaca agaaaaagat taaagacatc	420
tacgggaagg atgccttatt gcacgagcac tacgtttacg caaaggaggg ctatgagccc	480
gtgctcgta ttacagagtag tgaggactac gtcgagaata ccgagaaagc tctgaatgtg	540
tattacgaga tcggaaagat tctgtcccgg gatatactgt ccaaaatcaa ccagccatac	600
cagaaattcc ttgatgttct taacacaatc aaaaacgcgt cagatagcga cgggcaggat	660
cttctgttta caaatcaact caaggaacac cccactgatt tcagcgtgga gttcctcgag	720
cagaattcta acgaagtcca ggagggtgtc gccaaaggcat ttgcgtacta tatcgaaccc	780
cagcatcgcg atgtgctcca gctgtacgcc ccggaggcat ttaactacat ggacaaattc	840
aatgaacagg agattaatct gtctctggag gaactgaaag accagaggat gctctcccgg	900
tatgaaaagt gggaaaagat caaacagcat taccagcatt ggtccgactc cctgtcagaa	960
gagggggcgc gcctgttgaa aaagttgcag attcccatcg agcctaagaa agatgatata	1020
atacactctc taagccagga ggagaaggaa ctactgaagc ggatacaaat cgactcatcc	1080
gatttcctta gcacagaaga gaaggagttt ctaaaaaaac ttcagataga tattagagat	1140
tcactgagcg aggaagagaa ggagctgctc aaccgaattc aagtcgatag ttcgaacccc	1200
ttgtcagaaa aagagaagga attcctgaaa aagttgaagc tcgacatcca gccgtacgat	1260
attaatcagc ggctacaaga caccggcggt ctgattgata gcccagcat caaccttgac	1320
gtacggaaagc aatataagcg cgacattcaa aatatcgacg ccctattaca tcaatccata	1380
ggatccacgc tatacaataa aatctatcta tacgaaaaca tgaatattaa caatctcacc	1440

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gctacactgg gagcggacct ggtcgatagt acagacaaca caaagataaa cagaggtatt 1500
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 caggagtggg ataaagctct tggcttgcca aaatacacca aacttatcac ctttaatgtg 1860
 cacaacaggt atgcctctaa tatcgtcgag tcagcatacc tgattctcaa tgaatggaag 1920
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 tatggccgca cgaacgaggc tgaatTTTTT gcggaagcct ttagacttat gcacagcacc 2340
 gaccatgctg aaagggtgaa ggtgcaaaag aatgccccta aaaccttcca gttcataaat 2400
 gaccagatca agttcatcat caactcttga 2430

<210> 27

<211> 2427

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region

<400> 27

atgaatatta aaaaggagtt tattaaggtt atctctatgt cctgcttggt gacagcgata 60
 aactgtcag gaccagtgtt cataccctt gtccaggggg ccggcgggtca tggcgatgta 120
 ggtatgcatg tgaaagagaa ggaaaaaaat aaagacgaga acaagaggaa ggacgaggaa 180
 aggaataaga cccaagagga gcacctgaaa gagatcatga agcatattgt gaaaatcgag 240
 gtgaaggggg aagaggccgt gaaaaaagaa gcagctgaga agctgctaga gaaagtgcct 300
 tctgacgtcc tcgagatgta caaagcaatc ggcggcaaga ttacattgt tgatggtgac 360

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ataacaaagc atatctctct ggaggcctta agtgaagata agaaaaaat caaagacatt	420
tacggaaagg acgccctcct gcacgagcat tatgtctacg ctaaagaagg ctacgaaccc	480
gtgctcgtca tccagtcctc tgaggattat gtggagaaca ccgaaaaagc tttgaacgtc	540
tattacgaaa ttgggaaaat tctgtctaga gacattctca gcaagatcaa ccagccatac	600
caaaaattcc tagacgttct aaatacgatc aagaatgcca gtgactccga cgggcaggat	660
ctgttggtta cgaaccagct taaggagcat cctaccgatt tttctgtcga attccttgag	720
cagaactcca atgaagtcca agagggtctt gctaaggctt tcgcgtacta catcgagcct	780
cagcaccggg acgtgctgca gctctacgcc cctgaagctt tcaattatat ggacaagttc	840
aatgaacagg aaattaacct gagtttagaa gaactgaaag accaaagaat gttgtccaga	900
tacgagaagt gggagaagat caagcagcac tatcagcact ggtccgattc ccttagcgaa	960
gaagggcgcg ggctgcttaa aaagctgcag attccgatcg agccgaagaa agacgatata	1020
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gatttcctat ccacagagga aaaggaattt cttaaaaaac tccagattga tatacgggac	1140
tcattatctg aggaggaaaa ggaactcctg aaccggatcc aggtcgatag tagcaacccc	1200
ctgtcagaaa aggaaaagga gttctctaaa aaacttaagc tggatatcca accatacgac	1260
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ggaagtactc tttaacaaca aatctatctg tatgagaaca tgaatattaa taacctgact	1440
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gatacacgcg ccggttacct cgagaacggt aagttgatct tgcagcgaaa catcggactc	1680
gagattaagg atgtacagat catcaagcag agcgagaagg agtacattcg tatcgacgct	1740
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caagaatgga ataaagccct cggctctgcct aagtatacta agctaatac ctttaacgtg	1860
cacaatagat atgccagcaa tattgtcgag agcgcatacc taattctgaa cgaatggaaa	1920
aacaatatcc aaagcgacct gataaaaaag gtgactaatt atctcgttga tggcaatggc	1980
cgcttcgttt tcaccgatat tactctcccc aacatcgag aacagtacac tcatcaggac	2040
gagatttatg aacaggtgca cagtaagggg ctgtatgtcc ctgagagcgg ctctatcctt	2100
cttcacggac cctcaaaggg cgtagagtta aggaatgaca gcgaggggtt cattcacgag	2160
tttggccacg cagtggatga ttacgctgga tatctcctgg ataagaacca gtccgacctg	2220

-73-

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 tacggacgca caaatgagggc cgagtttttt gccgaagcgt tccgtttgat gcattcaacc 2340
 gaccacgcgg aaagactgaa agtgcagaaa aacgccccaa agacattcca gtttattaac 2400
 gaccaaataca agttcataat caattcg 2427

<210> 28

<211> 2427

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region

<400> 28

atgaatatta agaaagaatt cattaaagtc attagcatga gctgcctagt caccgccatc 60
 accctctctg gccagtggt tattccactg gtacagggcg caggcgggca tggcgacgtg 120
 ggaatgcatg ttaaggagaa ggaaaaaaat aaagatgaaa acaaacgcaa ggacgaagaa 180
 cggaacaaga cccaggagga gcacctgaaa gagatcatga aacacattgt gaaaatcgaa 240
 gttaaagggt aagaggccgt gaagaaggaa gccgcggaga aactgctgga aaaggtcccg 300
 tcggacgtac ttgaaatgta caaggcaatt ggtggcaaaa tctacattgt ggacggggac 360
 attaccaagc acataagcct ggaagcactc agcaggagca agaagaaaat aaaggacatt 420
 tacggaaagg acgctctgct ccacgagcac tatgtctacg cgaaggaggg gtacgagccc 480
 gtgttggtga tacagagttc cgaggactat gttgaaaata ctgaaaaagc cctcaacgtg 540
 tactatgaga ttggttaagat cttgtctaga gacatttctc gcaagattaa ccagccctac 600
 cagaaattcc tggatgtcct gaacacgatt aagaatgcct cagacagcga tggacaggac 660
 cttctgttta ccaatcagct taaagagcac cctaccgatt tctccgtgga attccttgag 720
 cagaattcaa atgagggtgca agaggtcttc gctaaggcct ttgcctacta ttcgagccc 780
 cagcatcgag acgtgctaca gttgtatgca ccagaagcct ttaactacat ggacaagttc 840
 aatgagcaag agatcaactt atcactggag gagctgaagg atcaacgcat gctgtctcgg 900
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 attcactcac tgtcccagga agagaaggag ctgcttaagc ggatccagat agattccagt 1080
 gacttcttaa gcacggaaga gaaggaatct ctgaaaaaat tgcagatcga tatccgtgat 1140

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tccctgtcag aggaggaaaa agaactgctg aaccggattc aggtggattc ctccaatcca 1200
ctgtccgaaa aggagaagga gtttttaaag aaactgaagc tcgatatcca gccttacgat, 1260
atcaatcaaa ggttgcagga cacaggggga ttgattgact cgcccagtat caacttggac 1320
gtgagaaagc agtacaaacg agacatacag aatatcgatg ctctcctgca tcaaagcatt 1380
gggtctacac tttaacaaca gatttatttg tacgaaaaca tgaatatcaa taatttgacc 1440
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caggagtggg ataaggctct cgggctgccc aagtacacaa agctgatcac attcaatgtt 1860
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tatggaagga ctaacgaggc agaattcttt gccgaagcct tccgcctgat gcattcaacc 2340
gaccacgcag agagactgaa agtgcagaaa aacgccccta agactttcca gtttattaat 2400
gaccagatca aatttatcat caactct 2427

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<210> 29

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 29

gagcttgata tcgccaccat ggatgc

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<210> 30

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 30

ccaccaatat ccgatgcatg gacttcgcg

29

<210> 31

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 31

cttgaaggat cctcaaccga tctcgtag

28

<210> 32

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR Primer

<400> 32

ccatgcatcg gatattggtg gctccgtg

30

<210> 33

<211> 21

<212> DNA

<213> Artificial Sequence

-76-

<220>

<223> Synthetic PCR primer

<400> 33

gtggacgacc aggaagtgat c

21

<210> 34

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 34

ggctatctgt ccagtacagc ttgaa

25

<210> 35

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 35

ccgtgctcgt tattcagagt

20

<210> 36

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 36

ccttctcttc tgtgctaagg

20

-77-

<210> 37

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 37

gaacctggat ccctacacca ccttggcgtc gatg

34

<210> 38

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 38

gctaattggat cctcaaaatg ccttggcgaa cacct

35

<210> 39

<211> 876

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region for Human/B. anthracis
antigen fusion protein

<220>

<221> CDS

<222> (13) .. (870)

<223>

<400> 39

-78-

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Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu	
1 5 10	
ctg tgt gga gca gtc ttc gtt tcg ccc agc gcc ggc ggg cat ggg gac	99
Leu Cys Gly Ala Val Phe Val Ser Pro Ser Ala Gly Gly His Gly Asp	
15 20 25	
gtt ggc atg cat gtg aaa gaa aag gag aaa aac aag gac gaa aac aag	147
Val Gly Met His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys	
30 35 40 45	
cgt aaa gac gaa gaa cgt aat aaa aca cag gag gaa cac tta aag gag	195
Arg Lys Asp Glu Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu	
50 55 60	
atc atg aag cac ata gta aag att gag gta aaa ggc gaa gag gct gta	243
Ile Met Lys His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val	
65 70 75	
aag aag gag gca gca gaa aaa ctg ttg gag aag gtg cct tct gac gtc	291
Lys Lys Glu Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val	
80 85 90	
tta gag atg tat aag gcc atc ggc ggt aag atc tat atc gtg gac gga	339
Leu Glu Met Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly	
95 100 105	
gac atc act aaa cac ata tct ctc gaa gct ctc tcc gag gac aag aaa	387
Asp Ile Thr Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys	
110 115 120 125	
aag att aaa gac atc tac ggg aag gat gcc tta ttg cac gag cac tac	435
Lys Ile Lys Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr	
130 135 140	
gtt tac gca aag gag ggc tat gag ccc gtg ctc gtt att cag agt agt	483
Val Tyr Ala Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser	
145 150 155	
gag gac tac gtc gag aat acc gag aaa gct ctg aat gtg tat tac gag	531
Glu Asp Tyr Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu	
160 165 170	
atc gga aag att ctg tcc cgg gac atc ctg tcc aaa atc aac cag cca	579
Ile Gly Lys Ile Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro	
175 180 185	
tac cag aaa ttc ctt gat gtt ctt aac aca atc aaa aac gcg tca gat	627
Tyr Gln Lys Phe Leu Asp Val Leu Asn Thr Ile Lys Asn Ala Ser Asp	
190 195 200 205	
agc gac ggg cag gat ctt ctg ttt aca aat caa ctc aag gaa cac ccc	675
Ser Asp Gly Gln Asp Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro	
210 215 220	
act gat ttc agc gtg gag ttc ctc gag cag aat tct aac gaa gtc cag	723
Thr Asp Phe Ser Val Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln	
225 230 235	
gag gtg ttc gcc aag gca ttt gcg tac tat atc gaa ccc cag cat cgc	771
Glu Val Phe Ala Lys Ala Phe Ala Tyr Tyr Ile Glu Pro Gln His Arg	

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240	245	250	
gat gtg ctc cag ctg tac gcc ccg gag gca ttt aac tac atg gac aaa			819
Asp Val Leu Gln Leu Tyr Ala Pro Glu Ala Phe Asn Tyr Met Asp Lys			
255	260	265	
ttc aat gaa cag gag att aat ctg tct ctg gag gaa ctg aaa gac cag			867
Phe Asn Glu Gln Glu Ile Asn Leu Ser Leu Glu Glu Leu Lys Asp Gln			
270	275	280	285
tga ggatcc			876

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Ala	Val	Phe	Val	Ser	Pro	Ser	Ala	Gly	Gly	His	Gly	Asp	Val	Gly	Met
			20					25					30		

His	Val	Lys	Glu	Lys	Glu	Lys	Asn	Lys	Asp	Glu	Asn	Lys	Arg	Lys	Asp
		35					40					45			

Glu	Glu	Arg	Asn	Lys	Thr	Gln	Glu	Glu	His	Leu	Lys	Glu	Ile	Met	Lys
		50				55					60				

His	Ile	Val	Lys	Ile	Glu	Val	Lys	Gly	Glu	Glu	Ala	Val	Lys	Lys	Glu
65					70				75						80

Ala	Ala	Glu	Lys	Leu	Leu	Glu	Lys	Val	Pro	Ser	Asp	Val	Leu	Glu	Met
				85					90					95	

Tyr	Lys	Ala	Ile	Gly	Gly	Lys	Ile	Tyr	Ile	Val	Asp	Gly	Asp	Ile	Thr
			100					105					110		

Lys	His	Ile	Ser	Leu	Glu	Ala	Leu	Ser	Glu	Asp	Lys	Lys	Lys	Ile	Lys
		115					120					125			

Asp	Ile	Tyr	Gly	Lys	Asp	Ala	Leu	Leu	His	Glu	His	Tyr	Val	Tyr	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

-80-

130	135	140
Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser Glu Asp Tyr 145 150 155 160		
Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys 165 170 175		
Ile Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys 180 185 190		
Phe Leu Asp Val Leu Asn Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly 195 200 205		
Gln Asp Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro Thr Asp Phe 210 215 220		
Ser Val Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln Glu Val Phe 225 230 235 240		
Ala Lys Ala Phe Ala Tyr Tyr Ile Glu Pro Gln His Arg Asp Val Leu 245 250 255		
Gln Leu Tyr Ala Pro Glu Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu 260 265 270		
Gln Glu Ile Asn Leu Ser Leu Glu Glu Leu Lys Asp Gln 275 280 285		

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<211> 35

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<210> 42

<211> 24

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<213> Artificial Sequence

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ctggagacac ctgtttatcg atcc

24

<210> 43

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<400> 43

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24

<210> 44

<211> 26

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gaagtactgg tctgtttaga tatggt

26

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accatatcta aacagaccag tacttc 26

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<212> DNA

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22

<210> 50

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23

<210> 51

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23

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tattggtggc ctgcagctct gc

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<210> 56

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<211> 24

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<210> 58

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<210> 59

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acacaatcat ccagccaagc gag

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<210> 62

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24

-87-

<210> 63

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<212> DNA

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<220>

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ccagagacag ctgaatctcc tggt

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<210> 69

<211> 25

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<210> 70

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23

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24

<210> 73

<211> 24

<212> DNA

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<223> Synthetic PCR primer

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<210> 75

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ggaagggagt cagctgactt cct

23

<210> 76

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 76

gcagatctgg atcctcaaga g

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